

GenCore version 4.5

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OM protein - protein search, using sw model

Run on: August 14, 2001, 05:33:23 ; Search time 15.69 Seconds
(without alignments)
1063.239 Million cell updates/sec

Title: US-09-599-400A-9
Perfect score: 1231
Sequence: 1 MGLSTVPDLLPLVLELLV.....ENVKTEDSGTTLPLVLRP 219
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1219	99.0	455	1 GORUT1	tumor necrosis fac
2	906.5	73.6	461	2 JC4302	tumor necrosis fac
3	879.5	71.4	454	1 GOMST1	tumor necrosis fac
4	867	70.4	461	1 GORTT1	tumor necrosis fac
5	216.5	17.6	435	2 I54182	tumor necrosis fac
6	202	16.4	427	1 GORUN	nerve growth facto
7	200	16.2	326	1 GQV2ML	T2 protein - myxom
8	189	15.4	325	2 B43692	T2 protein - rabbl
9	188	15.3	425	1 A26431	nerve growth facto
10	181	14.7	474	2 B38634	tumor necrosis fac
11	180.5	14.7	327	2 A46484	apoptosis-mediatin
12	176	14.3	459	2 I48954	gene murine tumour
13	174	14.1	305	2 A46476	B cell-associated
14	166.5	13.5	349	2 D72175	G2R protein - vari
15	164	13.3	348	2 T28623	hypothetical prote
16	164	13.3	349	2 D36858	gene G4R protein -
17	162.5	13.2	461	1 A35356	tumor necrosis fac
18	159.5	13.0	416	1 JN0006	nerve growth facto
19	154	12.5	677	2 C42125	trophozoite cystel
20	153.5	12.5	324	2 JC2395	Fas antigen precu
21	148	12.0	277	2 A60771	B-cell activation
22	143.5	11.7	1680	2 A43434	furin (EC 3.4.21.7
23	143	11.6	250	1 A49053	CD27 antigen precu
24	139.5	11.3	260	1 A46317	CD27 antigen precu
25	138	11.2	314	2 I37383	FAS soluble protei
26	137.5	11.2	335	2 A40036	apoptosis-mediatin
27	137.5	11.2	1548	2 S34583	serine proteinase
28	135.5	11.0	595	2 A42086	CD30 antigen precu
29	135	11.0	272	2 I48700	gene ox40 protein

30	132	10.7	899	2	G02428	subtilisin-like pr
31	132	10.7	915	2	JC6148	subtilisin-like pr
32	130.5	10.6	3672	2	T23433	hypothetical prote
33	130.5	10.6	3704	2	T37316	probable laminin a
34	126.5	10.3	271	2	S12783	Ox40 antigen precu
35	126.5	10.3	728	2	A48830	probable transcrip
36	124.5	10.1	277	2	I37552	Ox40 homolog - hum
37	122.5	10.0	192	2	T25513	hypothetical prote
38	121.5	9.9	1299	2	T43251	furin (EC 3.4.21.7
39	121	9.8	2321	2	S78549	notch3 protein - h
40	119	9.7	2318	2	S45306	notch 3 protein -
41	118.5	9.6	557	2	A48434	variant-specific s
42	118	9.6	596	2	A45664	variant-specific s
43	118	9.6	837	2	S43656	furin (EC 3.4.21.7
44	118	9.6	1790	1	NMFFB1	laminin beta-1 cha
45	118	9.6	2824	2	T22759	hypothetical prote

ALIGNMENTS

RESULT 1

GORUT1

tumor necrosis factor receptor 1 precursor [validated] - human
N:Alternate names: P55 tumor necrosis factor receptor; TNF receptor type 1
N:Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding prot
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence-revision 30-Jun-1992 #text-change 08-Dec-2000
C:Accession: A38208; A34899; A34900; A36555; A38281; S12057; JT0758; A60231;
R:Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
Genomics 13, 219-224, 1992
A:Title: Structure of the human TNF receptor 1 (p60) gene (TNFRF1) and localization to
A:Reference number: A38208; MUID:92250049
A:Accession: A38208
A:Molecule type: DNA
A:Residues: 1-455 <FUC>
A:Cross-references: GB:M75864; GB:M75865; GB:M75866; NID:g339748; PIDN:AAA61201.1; PI
R:Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Less
Cell 61, 351-359, 1990
A:Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor re
A:Reference number: A34899; MUID:90235284
A:Accession: A34899
A:Molecule type: mRNA
A:Residues: 1-455 <LOB>
A:Cross-references: GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36753.1; PID:g339754
A:Experimental source: placenta
A:Note: part of this sequence, including the amino end of the mature protein, confirm
R:Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga,
Cell 61, 361-370, 1990
A:Title: Molecular cloning and expression of a receptor for human tumor necrosis fact
A:Reference number: A34900; MUID:90235285
A:Accession: A34900
A:Molecule type: mRNA
A:Residues: 1-455 <SCH>
A:Cross-references: GB:M33294; NID:g339744; PIDN:AAA03210.1; PID:g339745
R:Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M
DNA Cell Biol. 9, 705-715, 1990
A:Title: Molecular cloning and expression of human and rat tumor necrosis factor rece
A:Reference number: A36555; MUID:91090841
A:Accession: A36555
A:Molecule type: mRNA
A:Residues: 1-455 <HIM>
A:Cross-references: GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756
A:Accession: C36555
A:Molecule type: protein
A:Residues: 30-38;41-53,'X',55-79,'XX',82-94,'NK','XX',100-104;107-128;162-167,'X',16
A:Note: the purified protein, called tumor necrosis factor binding protein, is a solu
R:Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
A:Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of
A:Reference number: A38281; MUID:91017509
A:Accession: A38281
A:Molecule type: mRNA

A:Residues: 1-455 <GRA>
A:Cross-references: GB:M37764
A:Note: The authors translated the codon TGG for residue 371 as Thr, AAG for residue 372 and TGG for residue 373. The authors also translated the codon TGG for residue 371 as Thr, AAG for residue 372 and TGG for residue 373.
R:Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann, E.M.B. J. 9, 3269-3278, 1990
A:Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type I form of the receptor.
A:Reference number: S12057; MUID:91006021
A:Accession: S12057
A:Molecule type: mRNA
A:Residues: 1-455 <NOR>
A:Cross-references: EMBL:X55133; NID:g37223; PIDN:CAA39021.1; PID:g37224
A:Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, were cloned from a cDNA library.
R:Kemper, O.; Wallach, D.
Gene 134, 209-216, 1993
A:Title: Cloning and partial characterization of the promoter for the human p55 tumor necrosis factor receptor.
A:Reference number: J70758; MUID:94085779
A:Accession: J70758
A:Molecule type: DNA
A:Residues: 1-113 <REM>
R:Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
Eur. J. Immunol. 20, 1167-1174, 1990
A:Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence, and characterization of an inhibitor (soluble tumor necrosis factor receptor).
A:Reference number: A60231; MUID:90292116
A:Accession: A60231
A:Molecule type: protein
A:Residues: 41-43, 'X', 45-53, 'X', 55-57 <SEC>
R:Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucchi III, J.A.; Jeffes, E.W.B.; Le Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A:Title: Purification and characterization of an inhibitor (soluble tumor necrosis factor receptor).
A:Reference number: A38258; MUID:91062364
A:Accession: A38258
A:Molecule type: protein
A:Residues: 41-60 <GAT>
A:Experimental source: cancer patient serum
R:Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.
Eur. J. Haematol. 42, 270-275, 1989
A:Title: Isolation and characterization of a tumor necrosis factor binding protein from human urine.
A:Reference number: A60594; MUID:89171156
A:Accession: A60594
A:Molecule type: protein
A:Residues: 41-43, 'X', 45-53, 'V', 55-57, 'XK', 60 <OLS>
A:Experimental source: renal failure patient urine
R:Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence for two distinct receptors.
A:Reference number: A35010; MUID:90110215
A:Accession: A35010
A:Molecule type: protein
A:Residues: 41-45 <ENG>
A:Experimental source: normal urine
R:Kajihara, J.; Asada, K.; Kirihara, S.; Kato, K.
Biochem. Biotechnol. Biochem. 58, 2266-2268, 1994
A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified from human urine.
A:Reference number: J02404; MUID:95128033
A:Accession: J02404
A:Molecule type: protein
A:Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAJ>
A:Experimental source: urine
C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
C:Genetics:
A:Gene: GDB:TNFR1
A:Cross-references: GDB:125913; OMIM:191190
A:Map position: 12p13.2-12p13.3
A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
A:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-21/Domain: signal sequence status predicted <SIG>
F:22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>
F:30-211/Domain: extracellular status predicted <EXT>
F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status predicted <MAT>
F:44-82/Domain: NGF receptor repeat homology <NGF>

F:84-126/Domain: NGF receptor repeat homology <NG2>
F:127-167/Domain: NGF receptor repeat homology <NG3>
F:168-196/Domain: NGF receptor repeat homology <NG4>
F:212-234/Domain: transmembrane #status predicted <MEM>
F:235-455/Domain: intracellular #status predicted <INT>
F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.0%; Score 1219; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.2e-82;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDRKDSVCPQGYIHPQNNISICT 60
Db 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDRKDSVCPQGYIHPQNNISICT 60

Qy 61 KCHKGTLYNDPCPGQDTCRECEGSFTASENHLRHLCSCKRKMGMQVEISSCTVD 120
Db 61 KCHKGTLYNDPCPGQDTCRECEGSFTASENHLRHLCSCKRKMGMQVEISSCTVD 120

Qy 121 RDTVCGCRKNOYRHWSENLFOCFNCISLCLNGTVHLSOEKQNTVCTCHAGFFLRENECV 180
Db 121 RDTVCGCRKNOYRHWSENLFOCFNCISLCLNGTVHLSOEKQNTVCTCHAGFFLRENECV 180

Qy 181 SCNSCKKSLCTKLCPLQIENVKGTEDSGTIVLLPLV 217
Db 181 SCNSCKKSLCTKLCPLQIENVKGTEDSGTIVLLPLV 217

RESULT 2
JC4302
tumor necrosis factor receptor p55 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999
C:Accession: JC4302; PC4093
R:Suter, B.; Pauli, U.
Gene 163, 263-266, 1995
A:Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.
A:Reference number: JC4302; MUID:96011645
A:Accession: JC4302
A:Molecule type: mRNA
A:Residues: 1-461 <SUT>
A:Cross-references: GB:U19994; NID:g1141752; PIDN:AAC48499.1; PID:g1141753
A:Accession: PC4093
A:Molecule type: protein
A:Residues: 1-7 <SU2>
A:Experimental source: kidney cell line 15
C:Genetics:
A:Gene: tnfr
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>
F:44-194/Domain: extracellular cysteine rich #status predicted <EXT>
F:44-82/Domain: NGF receptor repeat homology <NG1>
F:84-126/Domain: NGF receptor repeat homology <NGF>
F:211-231/Domain: transmembrane #status predicted <TMM>
F:361-447/Domain: signal transduction #status predicted <SIT>
F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 73.6%; Score 906.5; DB 2; Length 461;
Best Local Similarity 74.7%; Pred. No. 3.2e-59;
Matches 162; Conservative 16; Mismatches 38; Indels 1; Gaps 1;

Qy 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDRKDSVCPQGYIHPQNNISICT 60
Db 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDRKDSVCPQGYIHPQNNISICT 60

Qy 61 KCHKGTLYNDPCPGQDTCRECEGSFTASENHLRHLCSCKRKMGMQVEISSCTVD 120
Db 61 KCHKGTLYNDPCPGQDTCRECEGSFTASENHLRHLCSCKRKMGMQVEISSCTVD 120

Qy 121 RDTVCGCRKNOYRHWSENLFOCFNCISLCLNGTVHLSOEKQNTVCTCHAGFFLRENECV 180
Db 121 RDTVCGCRKNOYRHWSENLFOCFNCISLCLNGTVHLSOEKQNTVCTCHAGFFLRENECV 180

Qy 181 SCNSCKKSLCTKLCPLQIENVKGTEDSGTIVLLPLV 217
Db 181 SCNSCKKSLCTKLCPLQIENVKGTEDSGTIVLLPLV 217

QY 121 RDTVCGCRKNQYRHYWENLPOCNCSLCLNGTVHLSQEKQNTVCTCHAGFFLRENECV 180
Db 121 RDTVCGCRKNQYRHYWENLPOCNCSLCLNGTVHLSQEKQNTVCTCHAGFFLRENECV 180
QY 181 SCNCKKSLCTKCLPOIENKVKTESDGTAVLLPLV 217
Db 181 SCVNCKNA-DCKNLCPTATSETRNFQDTGTVLLPLV 216

RESULT 3
GOMST1
tumor necrosis factor receptor 1 precursor - mouse
N:Alternate names: tumor necrosis factor receptor, 55K
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence.revision 30-Jun-1992 #text_change 01-Dec-2000
R:Lewis, M.; Taggart, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor
A:Reference number: A38634; MUID:91187885
A:Accession: A38634
A:Molecule type: mRNA
A:Residues: 1-454 <LEW>
A:CROSS-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk
Mol. Cell. Biol. 11, 3020-3026, 1991
A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for
A:Reference number: A40254; MUID:91246168
A:Accession: A40254
A:Molecule type: mRNA
A:Residues: 1-454 <GO2>
A:CROSS-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R:Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissoneghis, A.M.; Gray, P.W.; Feldma
Eur. J. Immunol. 21, 1649-1656, 1991
A:Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis
A:Reference number: S16677; MUID:91285014
A:Accession: S16677
A:Molecule type: mRNA
A:Residues: 1-454 <BAR>
A:CROSS-references: EMBL:X59238; NID:g53578; PIDN:CAA41922.1; PID:g53579
R:Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
Immunogenetics 34, 338-340, 1991
A:Title: Molecular cloning and expression of the mouse Tnf receptor type b.
A:Reference number: S19021; MUID:92039815
A:Accession: S19021
A:Molecule type: mRNA
A:Residues: 1-454 <ROT>
A:CROSS-references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849
R:Bebo, B.F.
Immunogenetics 39, 450-451, 1994
A:Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell
A:Reference number: S154532; MUID:94245292
A:Accession: S154532
A:Molecule type: mRNA
A:Residues: 1-454 <RES>
A:CROSS-references: GB:L26349; NID:g430732; PIDN:AAA59361.1; PID:g430733
R:Rothe, J.G.; Bluetmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.
Mol. Immunol. 30, 165-176, 1993
A:Title: Genomic organization and promoter function of the murine tumor necrosis factor
A:Reference number: S157826; MUID:93156721
A:Accession: S157826
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-393,'G',395-454 <RES>
A:CROSS-references: GB:M76656; NID:g202100; PIDN:AAA40465.1; PID:g202102
C:Comment: This protein is one of two distantly related receptors for both TNF-alpha (ca
C:Genetics:
A:Gene: TNFR-2
A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protei
F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-454/Product: tumor necrosis factor receptor type 1 #status predicted <M>
F:30-212/Domain: extracellular #status predicted <EXT>
F:44-82/Domain: NGF receptor repeat homology <NG1>
F:84-126/Domain: NGF receptor repeat homology <NG2>
F:127-167/Domain: NGF receptor repeat homology <NG3>
F:168-204/Domain: NGF receptor repeat homology <NG4>
F:213-235/Domain: transmembrane #status predicted <MEM>
F:236-454/Domain: intracellular #status predicted <INT>
F:54,151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 71.4%; Score 879.5; DB 1; Length 454;
Best Local Similarity 71.6%; Pred. No. 3e-57;
Matches 156; Conservative 23; Mismatches 38; Indels 1; Gaps 1;

QY 1 MGLSTVPDLLPLVLELLVGYPSGVLPHLGDREKRDVCPQGYIHPQNNISICT 60
Db 1 MGLPTVPGLLLSLVLLALLMGTHPSGVTGLVPSLGDREKRDVCPQGYIHPQNNISICT 60
QY 61 KCHKTYLYNDPCPGQDTCRECESGSFASENHLRHLCSCKRKGQVEISSCTVD 120
Db 61 KCHKTYLVSDPCSPGRDTCVCEKEKGTFTASQNYLRQCLCKRKGQVEISSCTVD 120
QY 121 RDTVCGCRKNQYRHYWENLPOCNCSLCLNGTVHLSQEKQNTVCTCHAGFFLRENECV 180
Db 121 KDTVCGCKENQRYLSETHFCVDCSPCFNGTVPITPKETQNTVCTCHAGFFLRENECV 180
QY 181 SCNCKKSLCTKCLG-POIENKVKTESDGTAVLLPLV 217
Db 181 PCSHCKKNECKMKLCLPLPLANVTNPQDSGTAVLLPLV 218

RESULT 4

QORT1

tumor necrosis factor receptor 1 precursor - rat
N:Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence.revision 07-Oct-1994 #text_change 22-Jun-1999
C:Accession: B36555

R:Himmeler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M
DNA Cell Biol. 9, 705-715, 1990

A:Title: Molecular cloning and expression of human and rat tumor necrosis factor rece
A:Reference number: A36555; MUID:91090841

A:Accession: B36555

A:Molecule type: mRNA

A:Residues: 1-461 <HIM>

A:CROSS-references: GB:M63122; NID:g207361; PIDN:AAA42256.1; PID:g207362

C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin)

C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

C:Keywords: duplication; glycoprotein; receptor; transmembrane protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-461/Product: tumor necrosis factor receptor type 1 #status predicted <M>

F:30-211/Domain: extracellular #status predicted <EXT>

F:30-201/Product: tumor necrosis factor binding protein #status predicted <TBP>

F:44-82/Domain: NGF receptor repeat homology <NG1>

F:84-126/Domain: NGF receptor repeat homology <NG2>

F:127-167/Domain: NGF receptor repeat homology <NG3>

F:168-204/Domain: NGF receptor repeat homology <NG4>

F:212-234/Domain: transmembrane #status predicted <MEM>

F:235-461/Domain: intracellular #status predicted <INT>

F:54,151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 70.4%; Score 867; DB 1; Length 461;
Best Local Similarity 70.0%; Pred. No. 2.5e-56;
Matches 152; Conservative 21; Mismatches 44; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLELLVGYPSGVLPHLGDREKRDVCPQGYIHPQNNISICT 60
Db 1 MGLPTVPGLLLSLVLLALLMGTHPSGVTGLVPSLGDREKRDVCPQGYIHPQNNISICT 60
QY 61 KCHKTYLYNDPCPGQDTCRECESGSFASENHLRHLCSCKRKGQVEISSCTVD 120
Db 61 KCHKTYLVSDPCSPGRDTCVCEKEKGTFTASQNYLRQCLCKRKGQVEISSCTVD 120

[illegible]

R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E. Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor genes
A:Reference number: A38634; MUID:91187885
A:Accession: B38634
A:Molecule type: mRNA
A:Residues: 1-474 <LEW>
A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk Mol. Cell. Biol. 11, 3020-3026, 1991
A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for A:Reference number: A40254; MUID:91246168
A:Accession: A40254
A:Molecule type: mRNA
A:Residues: 1-474 <GOO>
A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R:Kisnerghis, M.; Fellowes, R.; Feldmann, M.; Chernaiovsky, Y. submitted to the EMBL Data Library, May 1995
A:Description: Characterization of the promoter region of the murine p75-TNF receptor.
A:Reference number: S54816
A:Accession: S54816
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-22 <KIS>
A:Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C:Keywords: cytokine receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
F:40-77/Domain: NGF receptor repeat homology <NG1>
F:79-120/Domain: NGF receptor repeat homology <NG2>
F:166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 14.7%; Score 181; DB 2; Length 474;
Best Local Similarity 31.7%; Pred. No. 2.7e-06;
Matches 51; Conservative 20; Mismatches 76; Indels 14; Gaps 8;
QY 44 CPQGYIHPNNISCTCKHKYLYNDPCPGQDTCRECSGSTASENHLRHCLSC- 102
DB 40 COISQEIYDRKAQMCCKAPPGQYKHF- NKTSDPVCADCEASMTQVWVNOFRTCLSCS 98
QY 103 SKCRKEMQVEISCTCKHKYLYNDPCPGQDTCRECSGSTASENHLRHCLSC- 157
DB 99 SSCYTD--QVETRACTKQNRVCACAGRYCALKTH--SGSCRCQMLSKGPGFGVASS 154
QY 158 COEKQNTVC--TCHAGFFLRENECVSCNCKSLCTKLCPL 197
DB 155 RAPNGNVLCKACAPGTF--SDTTSSTDVCRPHRICSLAIP 193

RESULT 11
A46484
apoptosis-mediating membrane-associated polypeptide Fas - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A46484; A47254
R:Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenkins, J. Immunol. 148, 1274-1279, 1992
A:Title: The cDNA structure, expression, and chromosomal assignment of the mouse Fas and A:Reference number: A46484; MUID:92148151
A:Accession: A46484
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-327 <WAT>
A:Cross-references: GB:M83649; NID:g193225; PIDN:AAA37593.1; PID:g193226
A:Experimental source: BM3 macrophage cell line
R:Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S. Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993
A:Title: Aberrant transcription caused by the insertion of an early transposable element A:Reference number: A47254; MUID:93189576
A:Accession: A47254

A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-96 <ADA>
A:Cross-references: GB:S56490; NID:g298505; PIDN:AAB25700.1; PID:g298506
A:Experimental source: MRL lpr/lpr
A>Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:1268 F:81-124/Domain: NGF receptor repeat homology <NG4>
C:Superfamily: NGF receptor repeat homology
C:Keywords: transmembrane protein
F:81-124/Domain: NGF receptor repeat homology <NG4>

Query Match 14.7%; Score 180.5; DB 2; Length 327;
Best Local Similarity 25.9%; Pred. No. 2.3e-06;
Matches 55; Conservative 24; Mismatches 94; Indels 39; Gaps 7;
QY 10 LPLPLVLELVGIPSGVIGLVPHLGDREK---RDSVCPQGYIHPNNISCTCKHKGT 66
DB 7 VLPVLVAGSOLRVHTQGTNSISLKLRRVHETDKNCSEGLY---QGGPFCCQCPQPK 63
QY 67 YLYNDPCPGQDTCRECSGSTASENHLR-HCLSCSKCRKEMQVEISCTVDRDTCV 125
DB 64 KVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKRCRRTCLDEEHGLEVETNCTLTQTK 123
QY 126 GCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSQCEKQNTVCTCHAGFFLRENECVSCNC 185
DB 124 KCRPDIYCD--SPGCEHCVCACSEHGTL- PCTATSN-----NC 161
QY 186 KKSLECTKLCPLQIENVKGTEDSGTTLPLV 217
DB 162 RKQSPRNLWLLTI-----LVLLIPLV 183

RESULT 12
I48854
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: I48854
R:Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A. Mamm. Genome 5, 726-727, 1994
A:Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A:Reference number: I48854; MUID:95178848
A:Accession: I48854
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-459 <RES>
A:Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology F:151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 14.3%; Score 176; DB 2; Length 459;
Best Local Similarity 31.1%; Pred. No. 6.2e-06;
Matches 50; Conservative 20; Mismatches 77; Indels 14; Gaps 8;
QY 44 CPQGYIHPNNISCTCKHKYLYNDPCPGQDTCRECSGSTASENHLRHCLSC- 102
DB 25 COISQEIYDRKAQMCCKAPPGQYKHF- NKTSDPVCADCEASMTQVWVNOFRTCLSCS 83
QY 103 SKCRKEMQVEISCTVDRDTCVGCRRNQY-----RHYWSENLFQCFNCSLCLNG-TVHLS 157
DB 84 SSCSTD--QVETRACTKQNRVCACAGRYCALKTH--SGSCRCQMLSKGPGFGVASS 139
QY 158 COEKQNTVC--TCHAGFFLRENECVSCNCKSLCTKLCPL 197
DB 140 RAPNGNVLCKACAPGTF--SDTTSSTDVCRPHRICSLAIP 178

RESULT 13
A46476
B cell-associated surface molecule CD40, long splice form - mouse
C:Species: Mus musculus (house mouse)

C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C:Accession: A46476; A46515
R:Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A:Title: Differential increase of an alternatively polyadenylated mRNA species of murine
A:Reference number: A46476; MUID:92105763
A:Accession: A46476
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-305 <TOR>
A:Cross-references: GB:M83312; NID:gl553058
A:Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIPI:75207)
A:Note: this translation is not annotated in GenBank entry M83312, release 113.0
R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne,
J. Immunol. 149, 3921-3926, 1992
A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A:Reference number: A46515; MUID:93094586
A:Accession: A46515
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-287, 'LV' <GRI>
A:Cross-references: GB:M83312; NID:gl553058; PIDN:AAB08705.1; PID:gl553059; GB:M94126; N
A:Experimental source: BALB/c, liver
A:Note: sequence extracted from NCBI backbone (NCBIPI:120357)
C:Comment: For an alternative splice form, see PIR:A46515.
C:Comment: For an alternative splice form, see PIR:A46476.
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: alternative splicing; transmembrane protein
F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 14.1%; Score 174; DB 2; Length 305;
Best Local Similarity 28.4%; Pred. No. 6.4e-06;
Matches 60; Conservative 30; Mismatches 91; Indels 30; Gaps 11;

QY 13 LVLELVGIVPSGIVGLPHLGRKDSVCPQGYIHPQNNISICTCKHKGTYLYNDC 72
Db 1 MVSPLRCLALW--GCLLTAVHLG---QCVTCSDKQYLH---DQCCDLCPGSGRLTSHC 51

QY 73 PPGQDTDCRECSGSTASENHLRHLCSCKRKGQVEISSCTVDRTVCGRNQY 132
Db 52 TAL-EKTOCHPCDSGEFSAQWNRIRCHQHRKCEPNOGLRVKKEGTAEISDTVCTCKEQ- 109

QY 133 RHYWSENLFOCFNCSCLNG-TVHLSQEQKQNTVC-TCHAGFFLREN---ECVSCSNCK 186
Db 110 -HTSKDCEACAOHTPCIPGFGVNMEMATFTDVTCHPCPGVGFNSQSLFEKYPWTSC 168

QY 187 -KSLECTKLCPLQIENVKGTEDSGTIVLLPL 216
Db 169 DKNLEVLQ-----KGT--SQTNVICGL 188

RESULT 14
D72175
G2R protein - variola minor virus (strain Garcia-1966)
C:Species: variola minor virus
C>Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
R:Accession: D72175
R:Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopan
submitted to GenBank, March 1998
A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
A:Reference number: A72150
A:Accession: D72175
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <SHC>
A:Cross-references: GB:Y16780; NID:g5830555; PIDN:CAB54798.1; PID:g5830759
A:Experimental source: strain Garcia-1966
C:Gene: G2R
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 13.5%; Score 166.5; DB 2; Length 349;
Best Local Similarity 26.7%; Pred. No. 2.5e-05;
Matches 46; Conservative 19; Mismatches 64; Indels 43; Gaps 9;

QY 44 CPQGYIHPQNNISICTCKHKGTYLYNDCPGQDTCRECSGSTASENHLRHLCS 103
Db 32 CKDTEY---KRHLCCLSCLPPGTGYASRLCDK-TNTQCTPCGSGTFTSRNHLPA 87

QY 104 -KCRKEMQVEISSCTVDRTVCGRKNQYRHYWSENLFOCF-----NCSLCLNGTVHLS 157
Db 88 GRCNS--NQVETRSCTNTHNRICECPGY-----CLLKSGSGCKACVSQT---- 131

QY 158 COEKQNTVCTCHAGFFLRENECVS---CSNC-----KKSLECTKLCPLQIEN 201
Db 132 -----KCGIGYVSGHTSVGDVICSPCGFGTYVTSVSTDKCEPVNN 174

RESULT 15
T28623
hypothetical protein G2R - variola major virus
C:Species: variola major virus
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C:Accession: T28623
R:Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Au
Nature 366, 748-751, 1993
A:Title: Potential virulence determinants in terminal regions of variola smallpox vir
A:Reference number: 220488; MUID:94088747
A:Accession: T28623
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-348 <MAS>
A:Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g439102
A:Experimental source: strain Bangladesh 1975
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 13.3%; Score 164; DB 2; Length 348;
Best Local Similarity 27.8%; Pred. No. 3.8e-05;
Matches 42; Conservative 17; Mismatches 54; Indels 38; Gaps 8;

QY 44 CPQGYIHPQNNISICTCKHKGTYLYNDCPGQDTCRECSGSTASENHLRHLCS 103
Db 31 CKDTEY---KRHLCCLSCLPPGTGYASRLCDK-TNTQCTPCGSGTFTSRNHLPA 86

QY 104 -KCRKEMQVEISSCTVDRTVCGRKNQYRHYWSENLFOCF-----NCSLCLNGTVHLS 157
Db 87 GRCNS--NQVETRSCTNTHNRICECPGY-----CLLKSGSGCKACVSQT---- 130

QY 158 COEKQNTVCTCHAGFFLRENECVS---CSNC 185
Db 131 -----KCGIGYVSGHTSVGDVICSPC 152

Search completed: August 14, 2001, 05:37:34
Job time: 251 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 14, 2001, 05:37:08 ; Search time 1190.68 seconds
(without alignments)
11094.045 Million cell updates/sec

Title: US-09-599-400A-1
Perfect score: 854
Sequence: 1 gactgagagccatagctgt:.....ggcgcagcagcaaatggg 854

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 1: gb_ba1.*
- 2: gb_ba2.*
- 3: gb_ba3.*
- 4: gb_in1.*
- 5: gb_in2.*
- 6: gb_in3.*
- 7: gb_om.*
- 8: gb_ov.*
- 9: gb_pat1.*
- 10: gb_pat2.*
- 11: gb_ph.*
- 12: gb_pl1.*
- 13: gb_pl2.*
- 14: gb_pl3.*
- 15: gb_pl4.*
- 16: em_ba1.*
- 17: em_ba2.*
- 18: em_fun.*
- 19: em_htgo_hum.*
- 20: em_htgo_inv.*
- 21: em_htgo_rod.*
- 22: em_htg_hum1.*
- 23: em_htg_hum2.*
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- 87: gb_pr3.*
- 88: gb_pr4.*
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- 90: gb_pr6.*
- 91: gb_pr7.*
- 92: gb_pr8.*
- 93: gb_pr9.*
- 94: gb_rol.*
- 95: gb_rol2.*
- 96: gb_in4.*
- 97: gb_pr10.*
- 98: em_ba3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	676.6	79.2	2050	97	HUMTNFRP
2	676.6	79.2	2062	9	A21522
3	676.6	79.2	2062	10	I43805
4	676.6	79.2	2087	97	HUMTNFR
5	676.6	79.2	2111	9	A26412
6	676.6	79.2	2111	97	HUMTNFRB
7	676.6	79.2	2161	9	AR096330
8	676.6	79.2	2161	93	HSTNFR1A
					M60275 Human tumor
					A21522 TNF alpha g
					I43805 Sequence 24
					M33294 Human tumor
					A26412 cDNA for (5
					M58286 Homo sapien
					AR096330 Sequence
					X55313 H.sapiens T

9	676.6	79.2	2175	9	A43873	A43873 Sequence 1
10	676.6	79.2	2175	9	A78738	A78738 Sequence 7
11	676.6	79.2	2175	9	AR041076	AR041076 Sequence 1
12	676.6	79.2	2175	10	I64751	I64751 Sequence 1
13	676.6	79.2	2176	9	A19907	A19907 Synthetic n
14	675	79.0	1331	9	A29103	A29103 H. sapiens m
15	675	79.0	2112	97	HUMTNFR	M63121 human tumor
16	664.6	77.8	2061	9	A20255	A20255 55kd recept
17	651	76.2	126928	10	I26928	I26928 Sequence 2
18	650	76.1	1368	9	A29098	A29098 Synthetic D
19	635.8	74.4	6896	9	AR031375	AR031375 Sequence
20	598.4	70.1	600	9	A20257	A20257 Synthetic n
21	595.2	69.7	600	10	I43808	I43808 Sequence 47
22	510	59.7	510	9	A21525	A21525 oligonucleo
23	503	58.9	504	9	A20713	A20713 Synthetic n
24	503	58.9	504	10	I43813	I43813 Sequence 56
25	501	58.7	501	10	I43786	I43786 Sequence 1
26	489	57.3	500	9	A20254	A20254 Synthetic n
27	483	56.6	483	9	A29099	A29099 Synthetic D
28	451.6	52.9	2004	7	SSU19994	UI9994 Sus scrofa
29	433.4	50.7	581	7	FCU72344	U72344 Felis catus
30	427.8	50.1	572	7	AF013955	AF013955 Canis fam
31	415.8	48.7	2130	95	RATNFR	M63122 Rat tumor n
32	408.8	47.9	1956	94	MUSTNFR2	M59377 Murine tumo
33	408.8	47.9	2048	94	MUSTNFR1	M60468 Mouse tumor
34	408.8	47.9	2063	94	MMP55R	X59238 Murine mrna
35	408.8	47.9	2086	94	BC004599	BC004599 Mus muscu
36	408.8	47.9	2154	94	MUSTNFX	I26349 Mus musculu
37	408.8	47.9	2179	94	MNTNFR5	U97796 Mouse mrna
38	407.8	47.8	2440	7	BTU90937	X09037 Bos taurus
39	377.8	44.2	477	9	A20263	A20263 Synthetic 53
40	377.8	44.2	477	10	I43811	I43811 Sequence n
41	372	43.6	372	9	A20253	A20253 Synthetic n
42	372	43.6	372	10	I43787	I43787 Sequence 3
43	357.2	41.8	474	9	A20259	A20259 Synthetic n
44	357.2	41.8	474	10	I43809	I43809 Sequence 49
45	312.4	36.6	462	9	A20261	A20261 Synthetic n

RESULT	1
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LOCUS	HUMTNFRP 2050 bp mRNA PRI 03-AUG-1993
DEFINITION	Human tumor necrosis factor receptor(TNF) mRNA, complete cds.
ACCESSION	M60275 M37764
VERSION	M60275.1 GI:339759
KEYWORDS	TNF receptor; transmembrane receptor; tumor necrosis factor receptor.
SOURCE	Human placenta, cDNA to mRNA.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Gray, P.W., Barrett, K.J., Chantry, D., Turner, M. and Feldman, M.
TITLE	Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of recombinant soluble TNF-binding protein
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384 (1990)
MEDLINE	91017509
COMMENT	Draft entry and computer-readable sequence for [Proc. Natl. Acad. Sci. U.S.A. (1990) In press] kindly submitted by P.W.Gray, 13-AUG-1990.
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	/db_xref="taxon:9606"
	/tissue_type="placenta"
sig_peptide	155..274
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/gene="TNF receptor"	
275..1513	
/product="TNF receptor"	
BASE COUNT	429 a 611 c 566 g 444 t
ORIGIN	
Query Match	79.2%; Score 676.6; DB 97; Length 2050;
Best Local Similarity	95.3%; Pred. No. 4.2e-178;
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;	
QY 1	gagtgagagccatagctgttgcatggcgctctccacgctgacgtgacgtgctgtgcc 60
DB 130	GAGTGAGAGGCCATAGCTGTGCGCATGGCGCTCTCCACCGTGCCTGACCTGTGCTGCC 189
QY 61	gctggtgctcctggaactgttggtggaatatatccctcaggggttatgtgactggtccc 120
DB 190	GTGTGTGTCCTCGAGAGCTGTGGTGGGAATATACCCCTCAGGGGTTATTGGAGTGGTCCC 249
QY 121	tcacctagggagcagaggaagagagatagtggtgtgtcccaaggaataatatccaccc 180
DB 250	TCACCTAGGGGACAGGAGAGAGACATAGTGTGTCCCAAGGAGAAATATATCCACCC 309
QY 181	tcacaaataattgattgtgtgtaccagtgtcccaaggaacacactactgttacaatgactg 240
DB 310	TCAAAATAATTGCTTGTGTACCAAGTGCCACAAAGGAACCTACTTGTACAAATGACTG 369
QY 241	tcaggccggggcagagacacagctgagggagtgatgagagcggtcctccaccgttc 300
DB 370	TCCAGCCCGGGCAGGATACGGACTGACGGAGTGTGAGAGCGGCTCTCTACCCGGTTC 429
QY 301	agaaaaccacctcagacactgcctcagctgtcccaatgccaaaggaataatgggtcaggt 360
DB 430	AGAAACACCTCAGACACTGCTCAGCTGCTCCAAATGCCGAAGGAATGGTCAAGT 489
QY 361	ggagatctcttcttgcacagtggaccgggacacccgtgtgtgtgctgaggaagaacagta 420
DB 490	GGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGCTGCAGGAAGAACCAGTA 549
QY 421	ccggcattattggaggagaaaaccttttccagtgtctcaattgacgctctgcctcaatgg 480
DB 550	CCGGCATTATTGGAGTGAACACCTTTTCCAGTGTCTCAATTCGAGCTCTGCTCCTCAATGG 609
QY 481	gacctgacctctcctgcagagagaacacacacgtgtgacactgacctgcacagttt 540
DB 610	GACCGTGCACCTCTCTCTCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGTTT 669
QY 541	ctttctaagagaaaaacagtggtgtctcctgtagtaactgttaagaaaaagcctggagtgac 600
DB 670	CYTCTTAAGAGAAAACGAGTGTGTCTCTCTCTAGTAGTGTAAAGAAAAGCCTGGAGTGCAC 729
QY 601	gaagtgtgctaccaccagattgagaatgttaagggcactgaggaactcagggaccacagtt 660
DB 730	GAAGTTGTGCTACCCACAGATTGAGAATGTTAAGGGCAGCTGAGGAGCTCAGGCACACAGT 789
QY 661	gctgttgccctggttcgtccctgagccctttttcacagtgacataagcagtttttttgg 720
DB 790	GCTGTGCCCCCGTGCATTTCTTGTGCTTTTATCCCTTTCCTCTCTCTCATTTGTTTT 849
QY 721	tttgttttgg 731

Db 850 AATGATCGCT 860

RESULT 2

A21522 262 bp mRNA PAT 26-JUL-1994

LOCUS TNF alpha gene.

DEFINITION A21522

ACCESSION A21522

VERSION A21522.1 GI:579599

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1. (bases 1 to 2062)

AUTHORS

JOURNAL Patent: GB 2246569-A 1 05-FEB-1992;

FEATURES Location/Qualifiers

source 1..2062

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155..1522 /gene="TNF alpha gene"

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BASE COUNT 429 a 617 c 573 g 443 t

ORIGIN

Query Match 79.2%; Score 676.6; DB 9; Length 2062;

Best Local Similarity 95.3%; Pred. No. 4.2e-178;

Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 gagtgaagagccatagctgtctggcattggccctctccaccgtgcctgacctgctgtgcc 60

Db 130 GAGTGAGAGGCCATAGCTGTCTGGCATGGGCTCTCCACCGTGCCTGACCTGCTGTGCC 189

QY 61 gctggtctctggagctgttggtgggaataaccctcagggttatgtgactgtgtccc 120

Db 190 GCTGGTCTCTCTGGAGCTGTGTGGGAATATACCCCTCAGGGGTTATTGGACTGTCCC 249

QY 121 tcacctaggggacagagagagagatagtggtgtccccaaggaaataatataccacc 180

Db 250 TCACCTAGGGACAGGAGAGAGATAGTGTGTCTCCCAAGGAATAATATATCCACCC 309

QY 181 tcaaaataattcgattgtctgacaaagtgcacaaaggaaacctactgtgacaatgactg 240

Db 310 TCAAAATAATTTCGATTTCGTACCAAGTGCCACAAAGAACCTACTTGTACAAATGACTG 369

QY 241 tcaggccggggacagatcacgactgacgagagtgagagcggtccttcacgcgttc 300

Db 370 TCCAGGCCGGGGACGATACGAGGACTGCAGGAGTGTGAGAGCGGCTCCTTACCGCTTC 429

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QY 361 ggagatctctctgacagtgagccgggacacgcgtgtgtggctgcaggaagaacagta 420

Db 490 GGAGATCTCTTCTTGACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAGAACCACTA 549

QY 421 ccggcattattggagtgaaacacctttccagtgcttcaattgagcctctctcctcaatgg 480

Db 550 CCGGCAATTATTGGAGTGAAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTCCCTCAATGG 609

QY 481 gacgtgacactctctctgcccaggagagaaacagagacacacgtgtgacacctgccaatgagttt 540

Db 610 GACCGTGACCTCTCCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGACAGTTT 669

QY 541 ctttctaagagaaaacgagtgctctctctctagtaactgttaagaaaagcctggagtgac 600

Db 670 CTTTCTAAGAGAAAACGAGTGCTCTCTGTAGTAACCTGTAAAGAAAGCCCTGGAGTGAC 729

QY 601 gaagtgtgctaccacagattgagaatgttaagggcactgagagactcagagcacacacagt 660

Db 730 GAAGTTGTGCTACCCAGATTGAGAAATGTAAGGACACTGAGGACTCAGGACACACAGT 789

QY 661 gctgtgcccctggttgcctgagcctttttcaagtgatgaagaagttttttttttttttt 720

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QY 721 ttgtttttgtt 731

Db 850 AATGATATCGCT 860

RESULT 3

I43805 2062 bp DNA PAT 07-OCT-1997

LOCUS

DEFINITION Sequence 24 from patent US 5633145.

ACCESSION I43805

VERSION I43805.1 GI:2468903

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1. (bases 1 to 2062)

AUTHORS Feldmann, M., Gray, P.W., Turner, M.J.C. and Brennan, F.M.

TITLE TNF alpha receptor-derived binding protein

JOURNAL Patent: US 5633145-A 24 27-MAY-1997;

FEATURES Location/Qualifiers

source 1..2062

BASE COUNT 429 a 617 c 573 g 443 t

ORIGIN

Query Match 79.2%; Score 676.6; DB 10; Length 2062;

Best Local Similarity 95.3%; Pred. No. 4.2e-178;

Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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Db 130 GAGTGAGAGGCCATAGCTGTCTGGCATGGGCTCTCCACCGTGCCTGACCTGCTGTGCC 189

QY 61 gctggtctctggagctgttggtgggaataaccctcagggttatgtgactgtgtccc 120

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Db 250 TCACCTAGGGACAGGAGAGAGATAGTGTGTCTCCCAAGGAATAATATATCCACCC 309

QY 181 tcaaaataattcgattgtctgacaaagtgcacaaaggaaacctactgtgacaatgactg 240

Db 310 TCAAAATAATTTCGATTTCGTACCAAGTGCCACAAAGAACCTACTTGTACAAATGACTG 369

QY 241 tcaggccggggacagatcacgactgacgagagtgagagcggtccttcacgcgttc 300

Db 370 TCCAGGCCGGGGACGATACGAGGACTGCAGGAGTGTGAGAGCGGCTCCTTACCGCTTC 429

QY 301 aaaaaaccactcagacactgcctcagctgtccaaatgccgaaaggaaatgggtcaggt 360

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Db 430 AGAAACACCTCAGACACTGCCTCAGCTGCTCCAAATGCCAAAGGAAATGGGTCAGGT 489
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Db 490 GGAGATCTCTTCTTGTGCACAGTGGACCGGACACCGCTGTGTGGCTGCAGGAAGAACCAGTA 549
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Db 790 GCTGTGCCCTGTGTCATTTCTTGTGCTTTCCTTTATCCCTCCCTTCATTCAGTGGTTT 849
Qy 721 ttgtttttgt 731
Db 850 AATGTATCGCT 860

RESULT 4
HUMTNFR 2087 bp mRNA PRI 10-NOV-1993
LOCUS Human tumor necrosis factor receptor mRNA, complete cds.
DEFINITION M33294
ACCESSION M33294
VERSION M33294.1 GI:339744
KEYWORDS cell surface receptor; tumor necrosis factor receptor.
SOURCE Human placenta, cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2087)
AUTHORS Schall,T.J., Lewis,M., Koller,K.J., Lee,A.L., Rice,G.C., Wong,G.H.,
Gatanaga,T., Granger,G.A., Lentz,R., Raab,H., Kohr,W.J. and
Goeddel,D.V.
TITLE Molecular cloning and expression of a receptor for human tumor
necrosis factor
JOURNAL Cell 61, 361-370 (1990)
MEDLINE 90235285
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
by T.Schall, 26-MAR-1990.
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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182..1549
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Query Match 79.2%; Score 676.6; DB 97; Length 2087;
Best Local Similarity 95.3%; Pred. No. 4.2e-178;
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Qy 241 tccagggccggggcaggtacacgactgcaggtgcagggagtgtagagcggtctctccacgcttc 300
Db 397 TCCAGGCCCGGGCAGGATACGACTGCAGGGAGTGTGAGAGCGGCTCTCTACCGCTTC 456
Qy 301 agaaaacacacctcagacactgcctcagctgctcccaatgccgaaggaatgggtcaggt 360
Db 457 AGAAAACACACCTCAGACACTGCCTCAGCTGCTCCAAATGCCAAAGGAAATGGTCAGGT 516
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Qy 481 gacctgcaacctctctgcagggagaaacagaaacacacacccgtgtgcacctgcacgtttt 540
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Qy 541 ctttctaagagaaaacagagtgctctcctctgtagtaactgtaagaaaagcctgagtgac 600
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Qy 721 ttgtttttgtt 731
Db 877 AATGTATCGCT 887

RESULT 5
A26412 2111 bp DNA PAT 26-APR-1995
LOCUS cDNA for (55kD TNF-BP) tumor necrosis factor binding protein from
DEFINITION patent EP04117563.
ACCESSION A26412
VERSION A26412.1 GI:904968
KEYWORDS synthetic construct.
SOURCE synthetic sequence.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 2111)
AUTHORS Brockhaus,M., Dombic,Z., Gentz,R., Lesslauer,W., Loetscher,H. and
Schlaeger,E.J.
TITLE TNF-binding proteins

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Qy	561	gctattgcccctgattcgctccctgagcctttttttcacagtgcatgaagcaggttttttttggtt	720
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Qy	721	ttgtttttgtt	731
Db	882	AATGTATCGCT	892
RESULT 6			
HUMTNFRB HUMTNFRB 2111 bp mRNA PRI 03-AUG-1993			
LOCUS Homo sapiens tumor necrosis factor receptor mRNA, complete cds.			
DEFINITION M58286 M33480			
ACCESSION M58286.1 GI:339753			
VERSION tumor necrosis factor receptor.			
KEYWORDS Human cell line HL60, cDNA to mRNA.			
SOURCE			
ORGANISM Homo sapiens			
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE 1 (bases 1 to 2111)			
AUTHORS Loetscher, H., Pan, Y.-C.E., Lahm, H.-W., Gentz, R., Brockhaus, M.,			
Tabuchi, H. and Lesslauer, W.			
TITLE Molecular cloning and expression of the human 55 kd tumor necrosis			
factor receptor			
JOURNAL Cell 61, 351-359 (1990)			
MEDLINE 90235284			
FEATURES			
source Location/Qualifiers			
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BASE COUNT 445 a 629 c 587 g 450 t			
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Query Match 79.2%; Score 676.6; DB 97; Length 2111;			
Best Local Similarity 95.3%; Pred. No. 4.2e-178;			
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;			
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Qy	61	gctggtctctgagctgttggtgggaatataccctcaggggttatgtgactggctcc	120
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BASE COUNT 459 a 642 c 604 g 456 t
ORIGIN

Query Match 79.2%; Score 676.6; DB 93; Length 2161;
Best Local Similarity 95.3%; Pred. No. 4.2e-178;
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 1 gagtggagggccatagctgtctggcatggcctctccaccgtgcctgacctgctgtgcc 60
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Qy 61 gctggtgctcctggagctgtgtgggaataataaccctcaggggtattggactggctcc 120
Db 291 GCTGTGTCTCTGGAGCTGTGGTGGGAATATACCCCTCAGGGGTATTGGACTGGTCCC 350

Qy 121 tcacctagggagcaggagagagatagtggtgtcccccaaggaaataatatcacacc 180
Db 351 TCACCTAGGGACAGGGAGAGAGATAGTGTGTCTCCCCAAGGAAATATATCCACCC 410

Qy 181 tcaaaataattcgatttgctgtaccgaagtgcacaaaggaaacctacttgtacaatgactg 240
Db 411 TCAAAATAATTTCGATTGCTGTACCAAGTGCCACAAAGAACCTACTTGTACAATGACTG 470

Qy 241 tccagggccggggcaggatacaggaactcaggagtgtagagcggtccttcacogcttc 300
Db 471 TCCAGGCCCGGGCAGGATACGAGCTCAGGGAGTGTGAGAGCGGCTCTTCAACCGTTTC 530

Qy 301 agaaaacaccctcagacactgctcagctgtgtccaaatgcgcaaggaaatgggtcaggt 360
Db 531 AGAAAACACCCTCAGACACTGCTCAGCTGTGTCCAAATGCCGAAAGGAAATGGGTCAAGT 590

Qy 361 ggagatcctcttcacagtgagccgggacaccgtgtgtgctgcagagaagaacagta 420
Db 591 GGAGATCTCTTCTTCACAGTGGACCGGACACCGGTGTGTGCTGCAGGAGAACAGTA 550

Qy 421 ccggcattattgagtgaacaccttttccagtgcttcaattgcagcctctgcctcaatgg 480
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Db 891 GCTGTTGCCCTGGTCATTTTCTTGTGCTTTCCTGCTTTATCCCTCCTCTTCATTTGTTT 950
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RESULT 9
LOCUS      A43873      2175 bp      DNA      PAT      06-MAR-1997
DEFINITION Sequence 1 from Patent EP0657536.
ACCESSION  A43873
VERSION    A43873.1 GI:2299022
KEYWORDS   ,
SOURCE     unidentified.
ORGANISM   unidentified.
REFERENCE  1 (bases 1 to 2175)
AUTHORS    Wallach,D., Brackebusch,C., Varfolomeev,E. and Batkin,M.
TITLE       Proteases capable of shedding the soluble TNF-receptor and TNF-R
            derived peptides and antibodies against the proteases inhibiting
            the shedding
JOURNAL     YEDA RES & DEV (IL)
            Patent: EP 0657536-A 1 14-JUN-1995;
COMMENT     Other publication ZA 9407962 951121
            Other publication JP 7194376 950801
            Other publication AU 7574294 950504
            Other publication CA 2133872 950413.
FEATURES    Location/Qualifiers
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ORIGIN

Query Match 79.2%; Score 676.6; DB 9; Length 2175;
Best Local Similarity 95.3%; Pred. No. 4.2e-178;
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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Qy 181 tcaaaataattcgatttgctgtaccgaagtgcacaaaggaaacctacttgtacaatgactg 240
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Best Local Similarity	95.3%	Pred. No. 4.2e-178;			
Matches 697; Conservative	0;	Mismatches 34;	Indels	0;	Gaps
Qy 1	gagtgagaggccatagctgtctggcatggcgctctccacgctgctgacctgctgctgccc	60			
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Qy 61	gctggtgctcctggagctgtgtgtggaatatataccccctcagggggttattggaactggtccc	120			
Db 291	GCTGGTCTCTCTGGAGCTGTGTGGGAATATACCCCTCAGGGGTATTATGGACTGGTCC	350			
Qy 121	tcacctaggagacaggagagagagatgctgtgtccccaaggaaaaatatatccacc	180			
Db 351	TCACCTAGGGACAGGAGAGAGATAGTGTGTGCCCAAGGAAATATATCCACCC	410			
Qy 181	tcaaaataattcgatttctgtaccagtgcccaaaaggaaactacttgtacaatgactg	240			
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Qy 301	agaaaaaccactcaagacacactcctcagctgctccaaatgcgaaaggaaatgggtcaggt	360			
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Qy 361	ggagatctctcttgccacagtggaacgggacaccgctgtgtggtgcaggagaaacacagta	420			
Db 591	GGAGATCTCTTTCACAGTGGACGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACAGTA	650			
Qy 421	ccggcattattggagtgaaacacctttccagtgcttcaattgcagcctctgcctcaatgg	480			
Db 651	CCGCGCATATTGGAGTGAAACACCTTTTCCAGTGCTTCAATTGACGACCTCTGCCTCAATGG	710			
Qy 481	gacgctgcacctctctgcagaggagaaacagacacacgctgtgcaactgcacatgcaggttc	540			
Db 711	GACCGTGCACCTCTCCCTGCCAGGAGAACACACCGTGTGCACCTGCCATGCAGGTTT	770			
Qy 541	cttctaaagaaaacagctgtgtctcctgtagttaactgtaaagaaagcctggagctcac	600			
Db 771	CTTCTTAAGAGAAACAGAGTGTCTCTCTGTAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG	830			
Qy 601	gaagtgtgctaccctccagattgagaaatgttaaggggcaactgaggactcaggaccacaggt	660			
Db 831	GAACTTGTGCTACCCAGATTGAGATGTTAAGGGCACCTGAGGACCTCAGGACCTCAGGACCT	890			
Qy 661	gctgttgcctcctggtcgtccctgagcctttttcaeaagtgcataaagcagttttttttgtt	720			
Db 891	GCTGTGCCCTCGCTCACTTTTCTTGTGCTTTTTCCTTTTATCCCTCTCTCTCAATGTTT	950			
Qy 721	ttgtttttgtt 731				
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RESULT 13					
LOCUS	A19907	2176 bp	DNA	PAT	04-OCT-1994
DEFINITION	Synthetic nucleotide sequence Type I TNF receptor gene.				
ACCESSION	A19907				
VERSION	A19907.1 GI:641222				
KEYWORDS	synthetic construct.				
SOURCE	synthetic construct				
ORGANISM	artificial sequence.				
REFERENCE	1 (bases 1 to 2176)				

AUTHORS Wallach,D.; Nophar,Y., Kemper,O., Engelmann,H., Brakebusch,C. and Aderka,D.
TITLE Expression of the recombinant tumor necrosis factor binding protein I (TBP-1)
JOURNAL Patent: EP 0433900-A 28 JUN-1991;
YEDA RESEARCH AND DEVELOPMENT COMPANY LIMITED

FEATURES Location/Qualifiers
source 1..2176

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QY 721 ttgtttttgtt 731
DB 951 AATGTATCGCT 961

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A29103

LOCUS A29103 1331 bp DNA PAT 03-JUL-1995
DEFINITION H.sapiens mRNA for TNF-binding polypeptide from patent EP0393438.
ACCESSION A29103
VERSION A29103.1 GI:1247517
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1331)
AUTHORS Hauptmann,R., Himmeler,A., Maurer-Fogy,I. and Stratowa,C.
TITLE TNF-receptor, TNF-binding protein and DNA coding therefor
JOURNAL Patent: EP 0393438-A 53 24-OCT-1990;
BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H

FEATURES Location/Qualifiers
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Best Local Similarity 95.2%; Pred. No. 1.1e-177;
Matches 696; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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DB 188 GAGTGAGAGGCCATAGCTGTCTGGCATGGGCTCTCCACCGTGGCTGCTGCTGCC 247
QY 61 gctgtgctcctggagctgttggtgggaataataccctcagggttattggactgtgcc 120
DB 248 ACTGGTGTCTCTGGAGCTGTGTGGTGGGAATATACCCCTCAGGGGTATTGGACTGGTCCC 307
QY 121 tcaactaggggacaggagaagagatagtggtgtccccaagaaataatatcaccc 180
DB 308 TCACCTAGGGACAGGAGAGAGATAGTGTGTCCCAAGGAAATATATCCACCC 367
QY 181 tcaaaataattcgattgctgtaccagtgcccaaggaaacctacttgtacaatgactg 240
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QY 301 agaaaacacacctcagacactgcctcagctgtccaaatgccgaaggaaatgggtcaggt 360
DB 488 AGAAACACCTCAGACACTGCTCCTCAATGCCGAAGAAATGGGTGAGT 547
QY 361 ggagatctcttctgcacagtgagccgggacacccgtgtgtgctgcaggaagaaccagta 420
DB 548 GGAGATCTCTTCTGACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTA 607
QY 421 ccggcattattggagtgaaaacctttccagtgcttcaattgcagcctctgcctcaatgg 480
DB 608 CCGCATATTGGAGTGAAACCTTTTCCAGTGTCTCAATTGCAACCTCTGCTCAATGG 667
QY 481 gaccgtgcacctctcctgcaggagaacacacacccgtgtgcacctgacctgcaggtttt 540
DB 668 GACCGTGACCTCTCTCTGCGAGGAGAAACAGACCCGTGTGCACCTGCCATGCCAGGTTT 727
QY 541 ctttctaagagaacacagtgctgtcctgtagtaactgtgaagaaacccctggagtgcac 600
DB 728 CTTTCTAAGAGAAACAGTGCTGTCTCTGTAGTAACGTGAAGAAAGCCCTGAGTGCAC 787
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Db 908 AATGATCGCT 918

RESULT 15
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LOCUS 2112 bp mRNA PRI 03-AUG-1993
DEFINITION Human tumor necrosis factor receptor (TNF receptor) mRNA, complete cds.
ACCESSION M63121 M75861
VERSION M63121.1 GI:339755
KEYWORDS tumor necrosis factor receptor.
SOURCE Human cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2112)
AUTHORS Himmler,A., Maurer-Fogy,I., Kroenke,M., Scheurich,P.,
pfizenmaier,K., Lantze,M., Olsson,I., Hauptmann,R., Stratowa,C. and
Adolf,G.R.
TITLE Molecular cloning and expression of human and rat tumor necrosis
factor receptor chain (p60) and its soluble derivative, tumor
necrosis factor-binding protein
JOURNAL DNA Cell Biol. 9, 705-715 (1990)
MEDLINE 91090841
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Job time: 2476 sec

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Best Local Similarity 95.2%; Pred. No. 1.2e-177;
Matches 696; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 gaggtagagccatagctgtctggcatggcgctctccacgcgtgcctgacctgtgtgccc 60
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Db 182 GAGTGAGAGCCATAGCTGTCTGGCATGGGCTCTCCACCGTGCCTGCCTGCTGCTGCC 241
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QY 61 gctgtgtcctggagctgttggggaataataccctcaggggttatggacctgtgcc 120
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Db 242 ACTGGTGCCTCGAGCTGTGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTCCC 301
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QY 121 tcacctagggagcagagagagatagctgtgtgtcccaaggaataatatccaccc 180
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Db 302 TCACCTAGGGGACAGGAGAGAGATAGTGTGTGTCCTCCCAAGGAATAATATCCACCC 361
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using 'sw model'

Run on: August 14, 2001, 05:38:08 ; Search time 127.44 Seconds
(without alignments)
4207.690 Million cell updates/sec

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Perfect score: 854
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Scoring table: IDENTITY NUC
Gapop: 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues
Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	676.6	79.2	2062	13	AAQ20973
2	676.6	79.2	2062	13	AAQ24440
3	676.6	79.2	2088	12	AAQ10883
4	676.6	79.2	2088	22	AAQ83946
5	676.6	79.2	2111	12	AAQ10955
6	676.6	79.2	2111	20	AAQ09170
7	676.6	79.2	2161	21	AAZ48475
8	676.6	79.2	2175	16	AAQ90513
9	675	79.0	1334	11	AAQ06282
10	675	79.0	2176	12	AAQ12215
11	673.4	78.9	2170	14	AAQ50870

12	667	78.1	2141	11	AAQ06285	Human Tumour Necro
13	651.6	76.3	1368	14	AAQ49932	Lambda-derived TNF
14	651.6	76.3	1368	21	AAQ95105	Human TNFR1 coding
15	651	76.2	6889	17	AAV15931	DHFR/intron (WTAS
16	635.8	74.4	6926	18	AAV04431	Vector pCDNA3-19G1
17	606.4	71.0	608	13	AAQ24441	Encodes truncated
18	515.4	60.4	1478	20	AAQ58150	Cadcf-fusion polype
19	514	60.2	1301	18	AAQ94022	CDNA for TBP(20-19
20	506	58.3	1147	18	AAQ94021	CDNA for TBP(20-19
21	503	58.9	504	13	AAQ24445	Encodes truncated
22	483	56.6	483	19	AAV41548	Human soluble tumo
23	483	56.6	483	19	AAV19801	Soluble tumour nec
24	483	56.6	483	20	AAV811732	Tumour necrosis in
25	483	56.6	483	22	AAQ83945	Human 30 kDa TNF 1
26	424.4	49.7	1049	18	AAQ94007	CDNA for TBP(20-16
27	424.4	49.7	1202	18	AAQ94008	CDNA for TBP(20-16
28	418	48.9	1674	21	AAQ50196	MALE fusion plasm
29	409.4	47.9	2173	11	AAQ06284	Rat Tumour Necrosi
30	377.8	44.2	477	13	AAQ24444	Encodes truncated
31	357.2	41.8	474	13	AAQ24442	Encodes truncated
32	329.6	38.6	5870	21	AAV15044	Nucleotide sequenc
33	312.4	36.6	339	19	AAV19804	Truncated stNFR, s
34	312.4	36.6	462	13	AAQ24443	Encodes truncated
35	308.2	36.1	333	19	AAV19805	Truncated stNFR, s
36	304.4	35.6	332	19	AAV19803	Truncated stNFR, s
37	294.6	34.5	315	19	AAV19806	Truncated stNFR, s
38	288	33.7	1497	21	AAZ50194	MALE fusion plasm
39	273.8	32.1	294	19	AAV19808	Truncated stNFR, s
40	264.6	31.0	285	19	AAV19807	Truncated stNFR, s
41	253.8	29.7	1464	21	AAZ50195	MALE fusion plasm
42	189.8	22.2	2254	21	AAQ95104	Partial human TNFR
43	163.6	19.2	1358	21	AAQ95103	Partial human TNFR
44	162.8	19.1	1027	12	AAQ10878	Partial sequence o
45	162.8	19.1	1027	22	AAQ83944	Genomic clone for

ALIGNMENTS

RESULT 1
AAQ20973
ID AAQ20973 standard; DNA; 2062 BP.
XX
AC AAQ20973;
XX
DT 11-MAY-1992 (first entry)
XX
DE TNF-alpha binding protein gene.
XX
KW Tumour necrosis factor alpha; autoimmune diseases; cachectin; ss;
XX extracellular domain.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
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TNF alpha receptor"
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XX GB2246569-A.
XX p55 TNF-R gene. H
XX Plasmid Tumour Nec
XX Type I TNF recepto
PD 05-FEB-1992.
XX p55 Tumour necrosi

PF 15-JUN-1990; 90GB-0013410.

XX PR 15-JUN-1990; 90GB-0013410.

XX PA (CHAR-) CHARING CROSS SUNLEY.

XX PI Feldman M, Gray P, Turner M, Brennan F;

XX WPI; 1992-043613/06.

XX P-PSDB; AAR20787.

XX New tumour necrosis factor alpha binding protein and polypeptide

PT - useful in treating cachexia, sepsis and auto immune diseases

PT e.g. rheumatoid arthritis

XX Disclosure; Fig 1; 25pp; English.

XX The sequence is that of DNA encoding tumour necrosis factor alpha

CC binding protein which was obtd. from a human placental cDNA library

CC in lambda gt11 using a probe (AAQ20974). The DNA also encodes the

CC extracellular domain of human TNF alpha receptor and as such it is

CC useful for treating diseases where TNF alpha is involved as a

CC causative agent, e.g. cachexia, sepsis and autoimmune diseases,

CC specifically rheumatoid arthritis. See also AAQ20974.

XX Sequence 2062 BP; 429 A; 616 C; 573 G; 444 T; 0 other;

SQ

Query Match

Best Local Similarity 95.3%; Pred. No. 1.8e-162;

Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 1 gactgagagccatagctgtctgcatggcctctccaccgtgctgacctgactgctcc 60

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Qy 61 gctggtgctctgagctgtgtgggaatataccctcaggggtattggactggtccc 120

Db 190 gctggtgctctgagctgtgtgggaatataccctcaggggtattggactggtccc 249

Qy 121 tcacctgagggagagagagagatagtggtgtccccaaggaataatataccacc 180

Db 250 tcacctgagggagagagagatagtggtgtccccaaggaataatataccacc 309

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Db 310 tcaaaataatcattgctgtaccacagtgccacaaagaaacctactgtacaatgactg 369

Qy 241 tccagggccgggagagatagcagctgagggagtgtagagcggtctctccacgcttc 300

Db 370 tccagggccgggagagatagcagctgagggagtgtagagcggtctctccacgcttc 429

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Qy 481 gaccgtgacacctctctcagcaggaagaaacacacccgtgtgacacctgacatgcagggttt 540

Db 610 gaccgtgacacctctctcagcaggaagaaacacacccgtgtgacacctgacatgcagggttt 669

Qy 541 ctttctaagagaagaacagtggtgtctctctgtagttaactgtaagaagaacgctggagtgac 600

Db 670 ctttctaagagaagaacagtggtgtctctctgtagttaactgtaagaagaacgctggagtgac 729

Qy 601 gaagtgtgctaccaccagattgagaatgttaaggggcactgaggactcaggcaccacagt 660

Db 730 gaagtgtgctaccaccagattgagaatgttaaggggcactgaggactcaggcaccacagt 789

Qy 661 gctgtgtgcccctggttcgctccctgagcctttttcacagtgcataaagcagttttttgtt 720

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Qy 721 tttgtttgttt 731

Db 850 aatgtatgct 860

RESULT 2

AAQ24440

ID AAQ24440 standard; DNA; 2062 BP.

XX AC AAQ24440;

XX DT 05-NOV-1992 (first entry)

XX DE Encodes TNF-alpha 55kD receptor.

XX KW tumour necrosis factor alpha; extracellular binding domain;

KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;

KW malaria; viral meningitis; graft versus host disease;

KW autoimmune disease; rheumatoid arthritis.

OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 156..1517

FT /*tag= a

FT /product= human TNF-alpha

FT mat_peptide 1265..1267

FT /*tag= b

FT /note= "3"

FT mat_peptide 1265..1267

FT /*tag= c

FT mat_peptide 1258..1260

FT /*tag= d

FT /codon= Seq"AAG", aa:Leu

FT mat_peptide 1433..1435

FT /*tag= e

FT /codon= Seq"GAC", aa:Asn

FT sig_peptide 156..274

FT /*tag= f

XX WO9207076-A.

XX PN 30-APR-1992.

XX PD 18-OCT-1991; 91WO-GB01826.

XX PF 18-OCT-1990; 90GB-0022648.

XX (CHAR-) CHARING CROSS SUNLEY RES CENT.

XX Brennan FM, Feldmann M, Gray PW, Turner MJC;

XX WPI; 1992-167156/20.

XX P-PSDB; AAR24000.

XX New polypeptide capable of binding human TNF alpha - comprises

PT first three cysteine-rich subdomains of TNF alpha receptor for

PT treating autoimmune disease, septic shock, HIV etc.

XX Claim 4; Fig 1; 43pp; English.

XX This sequence encodes human TNF-alpha 55kD receptor. A placenta cDNA
CC library in gt10 was screened with probe AAQ29236. Ten hybridising clones
CC were plaque purified and cDNA size determined by PAGE against an
CC Eco RI digested phage DNA. The inserts of two cDNA clones were then

CC sequenced. The coding region of the majority of the human TNF-alpha
CC 55kD receptor was isolated as an EcoRI fragment encoding 374 amino
CC acids, and cloned into a mammalian cell expression vector, resulting
CC in pTNFR. A derivative of the TNF-alpha receptor was produced by
CC engineering a termination codon just prior to the transmembrane
CC domain. PCR with primers AAQ29237.8 generated a 300bp
CC restriction fragment which was cloned into pTNFR, giving pTNFRcd.
CC DNA sequencing confirmed this contained the designed DNA sequence.
CC The TNF-alpha receptor expression plasmids were then transfected
CC into monkey COS-7 cells.
CC See also AAQ24440-51, AAR24000, AAR24080-84, AAR27585, AAQ29236-8
XX
XX Sequence 2062 BP; 429 A; 618 C; 572 G; 443 T; 0 other;

Query Match 79.2%; Score 676.6; DB 13; Length 2062;
Best Local Similarity 95.3%; Pred. No. 1.8e-162;
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 gagtgagagccatagctgtctggcatgtggcctctccacgtgcctgacctgctgtgcc 60
DB 130 gagtgagagccatagctgtctggcatgtggcctctccacgtgcctgacctgctgtgcc 189
QY 61 gctggtgctctgagctgtgtggtggaatataccctcaggggttattgagactgtccc 120
DB 190 gctggtgctctgagctgtgtggtggaatataccctcaggggttattgagactgtccc 249
QY 121 tcacctaggagcagagagagagatagtggtgtccccaaggaataatattccacc 180
DB 250 tcacctaggagcagagagagatagtggtgtccccaaggaataatattccacc 309
QY 181 tcaaaataatctgattgtctgaccagtgtcccaaggaataatattccacc 240
DB 310 tcaaaataatctgattgtctgaccagtgtcccaaggaataatattccacc 369
QY 241 tccagccggggcagagatagctgagggagtggtgagagcgtctcctccaccgttc 300
DB 370 tccagccggggcagagatagctgagggagtggtgagagcgtctcctccaccgttc 429
QY 301 agaaaaccacctcagacactgctcagctgtcctcaaatgccaaaggaataatggctcaggt 360
DB 430 agaaaaccacctcagacactgctcagctgtcctcaaatgccaaaggaataatggctcaggt 489
QY 361 ggaagatctcttgcacagtgcacgggacacgggtgtgtggtgcaggagaaacagta 420
DB 490 ggaagatctcttgcacagtgcacgggacacgggtgtgtggtgcaggagaaacagta 549
QY 421 ccggcattattgagtgaaaaacctttccagtgcttcaattgcagcctctgcctcaatgg 480
DB 550 ccggcattattgagtgaaaaacctttccagtgcttcaattgcagcctctgcctcaatgg 609
QY 481 gaccgtgcacctctcctgccagagagaacacacgctgtgcacctgacctgcaggttt 540
DB 610 gaccgtgcacctctcctgccagagagaacacacgctgtgcacctgacctgcaggttt 669
QY 541 ctttctaagagaaaaagagtggtctcctgtagtaactgtaagaaaaagcgtgagtgac 600
DB 670 ctttctaagagaaaaagagtggtctcctgtagtaactgtaagaaaaagcgtgagtgac 729
QY 601 gaagttgtgctaccacagattgagaatgttaaggcagctgaggaactcaggaccacag 660
DB 730 gaagttgtgctaccacagattgagaatgttaaggcagctgaggaactcaggaccacag 789
QY 661 gctgttgccctggttgcgtccctgagcctttttcagtgatcataagcagttttttgt 720
DB 790 gctgttgccctggttgcgtccctgagcctttttcagtgatcataagcagttttttgt 849
QY 721 ttgtttttgtt 731
DB 850 aatgtatcgt 860

RESULT 3

AAQ10883
ID AAQ10883 standard; cDNA; 2088 BP.
XX
XX AAQ10883;
XX AC
XX
DT 13-MAY-1991 (first entry)
XX
XX 30kD TNF inhibitor precursor gene in lambda-gtl0-7ctnfbp.
XX
XX Tumour necrosis factor; inhibitor; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 171..1536
FT /*tag= a
XX
XX AU9058976-A.
XX
XX 24-JAN-1991.
XX
XX 16-JUL-1990; 90AU-0058976.
XX
XX 07-FEB-1990; 90US-0479661.
PR 18-JUL-1989; 89US-0381080.
PR 11-DEC-1989; 89US-0450329.
XX
XX (SYNE-) SYNERGEN INC.
XX
XX WPI; 1991-073847/11.
DR P-PSDB; AAR10986.
XX
XX Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT and -beta, useful as therapeutic agent.
XX
XX Disclosure; Fig 21; 142pp; English.
XX
XX The sequence encodes the entire 30 kD TNF inhibitor. The clone from
CC which the sequence was obtd. was isolated from a cDNA library
CC prep'd. from RNA form U937 cells treated with PMA/PHA. The whole
CC gene can be inserted into expression vectors for prep'n. of TNF
CC inhibitor for use in the treatment of inflammatory and degenerative
CC diseases.
CC See also AAQ10878, AAQ10884 and AAQ10907.
XX
XX Sequence 2088 BP; 439 A; 626 C; 578 G; 445 T; 0 other;

Query Match 79.2%; Score 676.6; DB 12; Length 2088;
Best Local Similarity 95.3%; Pred. No. 1.8e-162;
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 1 gagtgagagccatagctgtctggcatgtggcctctccacgtgcctgacctgctgtgcc 60
DB 144 gagtgagagccatagctgtctggcatgtggcctctccacgtgcctgacctgctgtgcc 203
QY 61 gctggtgctctgagctgtgtggtggaatataccctcaggggttattgagactgtccc 120
DB 204 gctggtgctctgagctgtgtggtggaatataccctcaggggttattgagactgtccc 263
QY 121 tcacctaggagcagagagagatagtggtgtccccaaggaataatattccacc 180
DB 264 tcacctaggagcagagagagatagtggtgtccccaaggaataatattccacc 323
QY 181 tcaaaataatctgattgtctgaccagtgtccacaaaggaactctgtacaatgactg 240
DB 324 tcaaaataatctgattgtctgaccagtgtccacaaaggaactctgtacaatgactg 383
QY 241 tccagggccggggcagagatagcaggtgagagcgtcctcctcaccgcttc 300
DB 384 tccagggccggggcagagatagcaggtgagagcgtcctcctcaccgcttc 443
QY 301 agaaaaccacctcagacactgcctcagctgtcctcaaatgcgaaaggaatgggtcaggt 360

AC AAQ10955;
 XX 24-MAY-1991 (first entry)
 XX
 DE Encodes human 55kD TNF-binding protein.
 XX
 KW Tumour Necrosis Factor; binding proteins; septic shock;
 KW autoimmune glomerulonephritis; lymphokine; cytokine.
 XX
 FH Key Location/Qualifiers
 FT sig_peptide 187..273
 FT /*tag= a
 FT mat_peptide 274..1551
 FT /*tag= b
 FT /*product= 55kD TNF-BP
 XX
 PN EP417563-A.
 XX
 XX 20-MAR-1991.
 XX
 PF 31-AUG-1990; 90EP-0116707.
 XX
 PR 20-APR-1990; 90CH-0001347.
 PR 12-SEP-1989; 89CH-0003319.
 PR 08-MAR-1990; 90CH-0000746.
 XX
 PA (HOFF) HOFFMANN-LA ROCHE AG.
 XX
 XX Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
 PI Schlaefer EJ;
 XX
 DR WPI; 1991-081851/12.
 DR P-PSDB; AAR11082.
 XX
 PT Insoluble tumour necrosis factor binding proteins - and DNA
 PT encoding them, useful in pharmaceutical prods. and for antibody
 PT prodn.
 XX
 PS Claim 4; Fig 1; 26pp; German.
 XX
 CC Partial amino acid sequences were determined for the 55 and 75kD
 CC TNF-BPs (see AAR11072-R11081) and oligonucleotide primers were
 CC synthesised based on these partial sequences. The primers were used
 CC to produce a cDNA fragment for use as a probe to screen a human
 CC placental cDNA bank constructed in lambda gt11. Positive clones were
 CC identified and sequenced. DNA constructs comprising the TNF-BP coding
 CC sequence may also contain a fragment encoding a human Ig domain.
 CC Recombinant constructs are used to transform cells to confer
 CC improved TNF-binding properties.
 CC See also AAQ10956.
 XX
 SQ Sequence 2111 BP; 445 A; 628 C; 588 G; 450 T; 0 other;

Query Match 79.2%; Score 676.6; DB 12; Length 2111;
 Best Local Similarity 95.3%; Pred No. 1.8e-162;
 Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 1 gagtggagggccatagctgtctggcatggcctctccaccgtgcctgacctgctgccc 60
 |||||
 Db 162 gagtggagggccatagctgtctggcatggcctctccaccgtgcctgacctgctgccc 221
 |||||
 Qy 61 gctggtgctctcctggagctgttgggtgggaataaccctcagggggttattggactgctccc 120
 |||||
 Db 222 gctggtgctctcctggagctgttgggtgggaataaccctcagggggttattggactgctccc 281
 |||||
 Qy 121 tcacctaggggacaggaggaagagagatagtggtgtccccaaggaaaaatatatccacc 180
 |||||
 Db 282 tcacctaggggacaggaggaagagagatagtggtgtccccaaggaaaaatatatccacc 341
 |||||
 Qy 181 tcaaaataattcgtattgctgtaccagtgcacaaaggaacctactgttacaatgactg 240
 |||||
 Db 342 tcaaaataattcgtattgctgtaccagtgcacaaaggaacctactgttacaatgactg 401
 |||||

Qy 241 tccagggcccgggcaggagatacggactcaggaggagtgtagagcggtcctctccacgcttc 300
 |||||
 Db 402 tccagggcccgggcaggagatacggactcaggaggagtgtagagcggtcctctccacgcttc 461
 |||||
 Qy 301 agaaaaccactcagacacacgctcagctcctcaaatgccagaagaaaatgggtcaggt 360
 |||||
 Db 462 agaaaaccactcagacacacgctcagctcctcaaatgccagaagaaaatgggtcaggt 521
 |||||
 Qy 361 ggagatctctcttgcacagtggaccgggacacccgtgtgtggctgcaggaagaaccagta 420
 |||||
 Db 522 ggagatctcttgcacagtggaccgggacacccgtgtgtggctgcaggaagaaccagta 581
 |||||
 Qy 421 ccggcattattggagtgaataaccctttccagtggttccaattgcagcctctgcctcaatgg 480
 |||||
 Db 582 ccggcattattggagtgaataaccctttccagtggttccaattgcagcctctgcctcaatgg 641
 |||||
 Qy 481 gaccgtgcacctctcctgccaggagagaacacacgctgtgcacctgcctgcaggttt 540
 |||||
 Db 642 gaccgtgcacctctcctgccaggagagaacacacgctgtgcacctgcctgcaggttt 701
 |||||
 Qy 541 ctctctaagagaaaaacgagtgtctcctctagtaactgttaagaaaaacccctggagtgcac 600
 |||||
 Db 702 ctctctaagagaaaaacgagtgtctcctctagtaactgttaagaaaaacccctggagtgcac 761
 |||||
 Qy 601 gaagtgtgctaccacagattgagaatgttaagggcactgagactcaggcaccacagt 660
 |||||
 Db 762 gaagtgtgctaccacagattgagaatgttaagggcactgagactcaggcaccacagt 821
 |||||
 Qy 661 gctgtgccccctggttcctgcctgagccttttccacagtgcataagcagttttttgtt 720
 |||||
 Db 822 gctgtgccccctggttcctgcctgagccttttccacagtgcataagcagttttttgtt 881
 |||||
 Qy 721 ttgtttttgtt 731
 |||||
 Db 882 aatgtatcgt 892

RESULT 6
 AAZ09170.
 ID AAZ09170 standard; cDNA; 2111 BP.
 XX
 AC AAZ09170;
 XX
 DT 18-OCT-1999 (first entry)
 XX
 DE Human tumour necrosis factor binding protein cDNA.
 XX
 KW Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;
 KW anti-inflammatory; antimalarial; treatment; septic shock; inflammation;
 KW autoimmune glomerulonephritis; cerebral malaria; immune response;
 KW antagonist; diagnosis; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 187..1554
 FT /*tag= a
 FT /*product= "TNF binding protein"
 FT sig_peptide 187..273
 FT /*tag= b
 FT mat_peptide 274..1551
 FT /*tag= c
 XX
 PN EP939121-A2.
 XX
 PD 01-SEP-1999.
 XX
 PF 31-AUG-1990; 90EP-0116707.
 XX
 PR 20-APR-1990; 90CH-0001347.
 PR 12-SEP-1989; 89CH-0003319.
 PR 08-MAR-1990; 90CH-0000746.

XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
PI Schlaeeger E;

PI Schlaefer E:

XX
XX

DR WPI; 1999-480840/

DR P-PSDB; AAY30934.

XX New insoluble proteins, and fragments, that bind to tumor necrosis

PT factor, used to treat e.g. septic shock or cerebral malaria

PT

PT factor, used to treat e.g. septic shock or cerebral malaria

XX

PS
XX
CC This invention describes novel homogeneous insoluble proteins (I),
CC their (i)nsoluble fragments (Ia) and their salts that can bind tumour
CC necrosis factor (TNF). The products of the invention have
CC anti-inflammatory and antimalarial activity. (I) and (Ia) are used (i)
CC to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
CC glomerulonephritis, cerebral malaria, immune responses and inflammation),
CC (ii) to purify TNF, (iii) to identify TNF antagonists and (iv) for
CC diagnostic determination of TNF in body fluids. Antibodies raised against
CC (I) are used for affinity purification of (I). This sequence encodes
CC a tumour necrosis factor binding protein described in the method of
CC the invention.

CC This invention describes novel homogeneous insoluble proteins (I),

their (In)soluble fragments (Ia) and their salts that can

CC necrosis factor (TNF). The products of the invention have anti-inflammatory and antimalarial activity. (I) and (Ta) are used (i)

QY 361 ggagatctcttctgacagtgagaccggagacacacggtgtgtggtgacaggaagaccagta 420
 Db 591 ggagatctcttctgacagtgagaccggagacacacggtgtgtggtgacaggaagaccagta 650
 QY 421 ccggcattattggagtgaaacacctttccagctcttcaattgcagcctcctcccaatgg 480
 Db 651 ccggcattattggagtgaaacacctttccagctcttcaattgcagcctcctcccaatgg 710
 QY 481 gacggtgacacctctctgcccaggagaaacagacacacggtgtgacacctgcccagagttt 540
 Db 711 gacggtgacacctctctgcccaggagaaacagacacacggtgtgacacctgcccagagttt 770
 QY 541 ctttctaagagaaacagagtggtctctctgtagtaactgttaagaaacgctggagtgac 600
 Db 771 ctttctaagagaaacagagtggtctctctgtagtaactgttaagaaacgctggagtgac 830
 QY 601 gaagttgtgctacccacagattgagaattgtaagggaactgaggactcaggcaccacagt 660
 Db 831 gaagttgtgctacccacagattgagaattgtaagggaactgaggactcaggcaccacagt 890
 QY 661 gctgttccccctggtctcctgacgctctttccacagtgacataagcagttttttttgt 720
 Db 891 gctgttccccctggtctcctgacgctctttccacagtgacataagcagttttttttgt 950
 QY 721 ttgtttttgtt 731
 Db 951 aatgatcgct 961

RESULT 9

AAQ06282
 ID AAQ06282 standard; DNA; 1334 BP.

XX AC AAQ06282;

XX DT 29-JAN-1991 (first entry)

XX DE Plasmid Tumour Necrosis Factor-Binding Protein 15 cDNA insert.

XX KW Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
 pTNF-BP15; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 213..1325

XX FT /*tag= a

XX FT /product=TNF-BP

XX PN EP393438-A.

XX PD 24-OCT-1990.

XX PF 06-APR-1990; 90EP-0106624.

XX PR 21-JUN-1989; 89DE-3920282.

XX PR 21-APR-1989; 89DE-3913101.

XX PA (BOEH) BOEHRINGER INGELHEIMINT.

XX PI Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;

XX DR WPI; 1990-321987/43.

XX DR P-PSDB; AAR07449.

XX PT DNA encoding TNF binding protein and TNF- receptor - used in
 PT tumour treatment and to understand mechanisms to TNF action

XX PS Disclosure; Fig 1(1-3); 51pp; German.

XX CC pTNF-BP15 is one of 30 positives clones in a screened cDNA library
 CC from induced TNF-induced fibrosarcoma cells. A TNF-BP had been
 CC isolated from the urine of patients with uraemia and probes/primers

CC were constructed from the determined amino acid sequence.
 CC To produce a vector expressing a soluble form of TNF-binding
 CC protein, this plasmid was cut with XmnI, amplified by PCR and the
 CC amplified DNA cut with BamHI and EcoRI.
 CC The resulting 0.75 kb DNA fragment was inserted into pT7/73 alpha-19
 CC (BRL) cut with the same enzymes to recover pTNF-BP. This was cut
 CC with BamHI and EcoRI, and the recovered fragment inserted into
 CC PAD-CMV1 (AAQ06283) to give the required plasmid pADTNF-BP.
 CC See also AAQ06282-Q06285.

XX SQ Sequence 1334 BP; 299 A; 409 C; 342 G; 284 T; 0 other;

Query Match 79.0%; Score 675; DB 11; Length 1334;

Best Local Similarity 95.2%; Pred. No. 3.9e-162;

Matches 696; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 gagttagagagccatagctgtgcatggcgctctccacgtgcctgacctgtgtgtgccc 60

Db 188 gagttagagagccatagctgtgcatggcgctctccacgtgcctgacctgtgtgtgccc 247

QY 61 gctgtgtcctctggagctgttggggaaataaccctcagggtttattggactgtccc 120

Db 248 actgtgtcctctggagctgttggggaaataaccctcagggtttattggactgtccc 307

QY 121 tcaccttagggacagggagagagatagtggtgtcccccaaggaaataatcacccc 180

Db 308 tcaccttagggacagggagagagatagtggtgtcccccaaggaaataatcacccc 367

QY 181 tcaataaattcgtgtaccagtgtcccaaggaaacacactctgtacaaactgactg 240

Db 368 tcaataaattcgtgtaccagtgtcccaaggaaacacactctgtacaaactgactg 427

QY 241 tccaggcccgggcaggacacgactgcaggagtggtgagagcggtccttaccgcgttc 300

Db 428 tccaggcccgggcaggacacgactgcaggagtggtgagagcggtccttaccgcgttc 487

QY 301 agaaaacacccacagacactgcctcagctgctccaaatgccaaaggaaatgggtcaggt 360

Db 488 agaaaacacccacagacactgcctcagctgctccaaatgccaaaggaaatgggtcaggt 547

QY 361 ggagatctcttctgacagtgagaccgggacacccgtgtgtggtgcaggagaaccagta 420

Db 548 ggagatctcttctgacagtgagaccgggacacccgtgtgtggtgcaggagaaccagta 607

QY 421 ccggcattattggagtgaaacaccttttccagtgcttcaattgcagcctcctcccaatgg 480

Db 608 ccggcattattggagtgaaacaccttttccagtgcttcaattgcagcctcctcccaatgg 667

QY 481 gaccgtgacacctctctgccaggagaaacagacacccgtgtgacactgccatgcaggttt 540

Db 668 gaccgtgacacctctctgccaggagaaacagacacccgtgtgacactgccatgcaggttt 727

QY 541 ctttctaagagaaacagagtggtgtctcctgtagtaactgttaagaaacgctggagtgac 600

Db 728 ctttctaagagaaacagagtggtgtctcctgtagtaactgttaagaaacgctggagtgac 787

QY 601 gaagttgtcctacccacagattgagaattgtaagggaactgaggactcaggcaccacagt 660

Db 788 gaagttgtcctacccacagattgagaattgtaagggaactgaggactcaggcaccacagt 847

QY 661 gctgttgccccctggttccctcagccttttccacagtgacataagcagttttttttgt 720

Db 848 gctgttgccccctggttccctcagccttttccacagtgacataagcagttttttttgt 907

QY 721 ttgtttttgtt 731

Db 908 aatgatcgct 918

RESULT 10

AAQ12215

ID AAQ12215 standard; DNA; 2176 BP.

```
XX AC AAQ12215;
XX 12-SEP-1991 (first entry)
XX Type I TNF receptor.
XX Tumour Necrosis Factor; TNF; binding protein; TBP-I; ss.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
FT terminator 244..246
FT FT /*tag= a
FT CDS /*note= "in-frame termination codon"
FT FT 256..1620
FT FT /*tag= a
FT FT /product= type I TNF receptor
FT sig_peptide 256..318
FT FT /*tag= b
FT mat_peptide 319..1620
FT FT /*tag= c
FT misc_rna 319..864
FT FT /*tag= d
FT FT /label= soluble_domain
FT FT /*note= "may be 2 codons shorter or a few codons
FT FT longer"
FT misc_feature 376..414
FT FT /*tag= e
FT FT /*note= "TBP-I derived sequence"
FT misc_feature 583..627
FT FT /*tag= f
FT FT /*note= "TBP-I derived sequence"
FT misc_feature 850..858
FT FT /*tag= g
FT FT /*note= "TBP-I derived sequence"
FT misc_rna 889..957
FT FT /*tag= h
FT FT /label= transmembrane_domain
FT repeat_unit 385..504
FT FT /*tag= i
FT FT /number= 1
FT repeat_unit 505..633
FT FT /*tag= j
FT FT /number= 2
FT repeat_unit 634..756
FT FT /*tag= k
FT FT /number= 3
FT repeat_unit 757..858
FT FT /*tag= l
FT FT /number= 4
FT polyA_signal 2145..2150
FT FT /*tag= m
XX PN EP433900-A.
XX 26-JUN-1991.
XX 13-DEC-1990; 90EP-0124133.
XX 12-JUL-1990; 90IL-0095064.
XX 13-DEC-1989; 89IL-0092697.
XX (YEDA ) YEDA RES & DEV CO LTD.
XX Wallach D, Nophar Y, Kemper O, Engelmann H, Brakebusch C;
XX Aderka D;
XX WPI; 1991-186774/26.
XX P-PSDB; AAR12550.
XX Recombinant tumour necrosis factor binding protein I - prepd. by
XX transfecting eukaryotic cells with vector contg. deoxyribonucleic
```

```
PT acid encoding human type T TNF receptor or soluble domain
XX Disclosure; Fig 1(D); 30pp; English.
XX The Tumour Necrosis Factor Binding Protein I is the soluble form of
XX type I TNF-receptor and constitutes a fragment of the cell surface
XX form of this receptor, corresp. to its extracellular domain.
XX There is no characteristic poly(A) addition signal near the 3' end
XX of the cDNA. The sequence ACTAAA (tag m) may serve as an
XX alternative to this signal, but with low efficiency.
XX See also AAQ12212-15.
XX Sequence 2176 BP; 475 A; 644 C; 602 G; 455 T; 0 other;
SQ
Query Match 79.0%; Score 675; DB 12; Length 2176;
Best Local Similarity 95.2%; Pred. No. 4.6e-162;
Matches 696; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 1 gagtgaagagccatagctgtcgtgcatggcgctctccacgctgctgactgctgctgcc 60
Db |||||
QY 231 gagtgaagagccatagctgtcgtgcatggcgctctccacgctgctgactgctgcc 290
Db |||||
QY 61 gctggtgctcctggagctgtgtgtgggaatataccctcaggggttattgactggtccc 120
Db |||||
QY 291 gctggtgctcctggagctgtgtgtgggaatataccctcaggggttattgactggtccc 350
Db |||||
QY 121 tcacctagggagagagagagagagatagtgtgtcccaagaaaatatatccacc 180
Db |||||
QY 351 tcacctagggagagagagagagatagtgtgtcccaagaaaatatatccacc 410
Db |||||
QY 181 tcaataataatcgtattgtgtacaaagtcacaaaggaacacctactgtacaatgactg 240
Db |||||
QY 411 tcaataataatcgtattgtgtacaaagtcacaaaggaacacctactgtacaatgactg 470
Db |||||
QY 241 tccaggcccggggcagagatagcaggactgcaggagtggtgagagcgctctcaccgcttc 300
Db |||||
QY 471 tccaggcccggggcagagatagcaggactgcaggagtggtgagagcgctctcaccgcttc 530
Db |||||
QY 301 agaaaaccacctcagacactgcctcagctcctcaaatgcgaagaaaatgggtcaggt 360
Db |||||
QY 531 agaaaaccacctcagacactgcctcagctcctcaaatgcgaagaaaatgggtcaggt 590
Db |||||
QY 361 ggagatctctctgcacagtggacccgggacacccgtgtgtgctgcaggaagaccagta 420
Db |||||
QY 591 ggagatctctctgcacagtggacccgggacacccgtgtgtgctgcaggaagaccagta 650
Db |||||
QY 421 ccggcattattggagtgaataacccctttccagtgcttcaattgcagcctctgcctcaatgg 480
Db |||||
QY 651 ccggcattattggagtgaataacccctttccagtgcttcaattgcagcctctgcctcaatgg 710
Db |||||
QY 481 gaccgtgacacctctcctgccaggagaaaacagacacccgtgtgcacccctgcactgaggttt 540
Db |||||
QY 711 gaccgtgacacctctcctgccaggagaaaacagacacccgtgtgcacccctgcactgaggttt 770
Db |||||
QY 541 ctcttaagagaaaacgagtgctcctcctgtagttaactgttaagaaaagcctggagtgac 600
Db |||||
QY 771 ctcttaagagaaaacgagtgctcctcctgtagttaactgttaagaaaagcctggagtgac 830
Db |||||
QY 601 gaagtgtgctaccaccagattgagaattgaaggcgactgagactcagcagccacacagt 660
Db |||||
QY 831 gaagtgtgctaccaccagattgagaattgaaggcgactgagactcagcagccacacagt 890
Db |||||
QY 661 gctgttgccctgggttcctcctgagcctttttcacagtgatagaagcagttttttgttt 720
Db |||||
QY 891 gctgttgccctgggttcctcctgagcctttttttgtgtgttttttttttttttttttttt 950
Db |||||
QY 721 ttgttttttttttttttttttttttttttttttttttttttttttttttttttttttttt 731
Db |||||
QY 951 aatgtatcgt 961
Db |||||
RESULT 11
```

```
AAQ50870
ID AAQ50870 standard; DNA; 2170 BP.
XX
AC AAQ50870;
XX
DT 13-MAY-1994 (first entry)
XX
DE p55 Tumour necrosis factor receptor coding sequence.
XX
KW TNF; tumour necrosis factor; receptor; disease; autoimmunity;
KW rheumatoid arthritis; graft rejection; graft vs. host; septic shock;
KW effector protein; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 256..1623
FT /*tag= a
FT /product= p55 Tumour necrosis factor receptor.
XX
PN EP568925-A.
XX
PD 10-NOV-1993.
XX
PF 29-APR-1993; 93EP-0106981.
XX
PR 03-MAY-1992; 92IL-0101769.
XX
PS (YEDA ) YEDA RES & DEV CO LTD.
XX
PI Brakebusch C, Wallach D;
XX
DR WPI; 1993-353057/45.
XX
DR P-PSDB; AAR42197.
XX
PT Modulating activity of tumour necrosis factor receptor - using
PT peptides(s), antibodies, etc. which interact with critical regions
PT of receptor or effector protein, for controlling auto-immune
PT disease, septic shock, etc.
XX
PS Claim 2; Figure 1; 17pp; English.
XX
CC Modification of the tumour necrosis factor receptor by mutation or
CC deletion modulates signal transduction and/or cleavage effected by
CC the receptor. This modulation of activity can also be achieved
CC using effector proteins which interact with the TNF receptor.
CC Molecules which interact with the TNF receptor or the effector
CC proteins can be used to treat or prevent diseases associated with
CC TNF activity e.g. autoimmune disease; rheumatoid arthritis; graft
CC rejection; graft vs. host disease or septic shock. They can also
CC be used to treat overdoses of exogenous TNF.
XX
SQ Sequence 2170 BP; 474 A; 657 C; 584 G; 455 T; 0 other;

Query Match 78.9%; Score 673.4; DB 14; Length 2170;
Best Local Similarity 95.1%; Pred. No. 1.2e-161;
Matches 695; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 gagtggagggccatagctgtctggcgtggcctctccaccgtgacctgctgctgcc 60
   |||||
DB 231 gagtggagggccatagctgtctggcgtggcctctccaccgtgacctgctgctgcc 290

QY 61 gctggtgctcctggagctgttgggtgggaataaccctcagggttattggactggctcc 120
   |||||
DB 291 gctggtgctcctggagctgttgggtgggaataaccctcagggttattggactggctcc 350

QY 121 tcacctaggggacaggagagagatagtggtgtccccaaggagaaatatatccacc 180
   |||||
DB 351 tcacctaggggacaggagagagatagtggtgtccccaaggagaaatatatccacc 410

QY 181 tcaaaataattcgtattgctgtaccagtgcacaaaggaaacctactgtacaatgactg 240
   |||||
```

RESULT	13
AAQ49932	
ID	AAQ49932 standard; cDNA to mRNA; 1368 BP.
XX	
XX	AAQ49932;
XX	
XX	29-APR-1994 (first entry)
XX	
XX	Lambda-derived TNF-R cDNA.
XX	
KW	Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
KW	IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW	rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW	pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW	graft verses host disease; sepsis; inflammation; allergy;
KW	autoimmune dysfunction; ss.
OS	Homo sapiens.
OS	Lambda-gt10-7-ctnfbp.
XX	
FH	Key Location/Qualifiers
FT	CDS 1..1366
FT	/*tag= a
FT	sig_peptide 1..120
FT	/*tag= b
FT	mat_peptide 121..1363
FT	/*tag= c
XX	W09319777-A.
PN	
XX	
PD	14-OCT-1993.
XX	
XX	26-MAR-1993; 93WO-US02938.
PF	
XX	
PR	30-MAR-1992; 92US-0860710.
XX	
PA	(IMMV) IMMUNEX CORP.
XX	
PI	Smith CA;
XX	
DR	WPI: 1993-336592/42.
DR	P-PSDB; AAR42059.
XX	
XX	New fusion protein tumour necrosis factor and human interleukin-1
PT	receptor - useful in therapy, diagnosis and assays of e.g.
PT	rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
XX	
PS	Disclosure; Page 57-59; 85pp; English.
XX	
CC	The sequences given in AAQ49931-32 encode human tumour necrosis factor
CC	receptor (TNF-R) and the sequences in AAQ49933-34 encode human
CC	interleukin-1 receptor (IL-1R). These sequences were used in the
CC	production of a fusion protein which conformed to one of the
CC	formulae:
CC	TNF-R-linker-TNF-R-linker-IL-1R
CC	IL-1R-linker-TNF-R-linker-TNF-R or
CC	TNF-R-linker-TNF-R
CC	The linker may comprise 5-100 amino acids selected from Gly, Asp,
CC	Ser, Thr and Ala. These linkers separate the individual moieties
CC	by such a distance that each component of the fusion protein is
CC	capable of folding into the secondary or tertiary structure required
CC	for its biological activity. These fusion proteins may be used in
CC	therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC	particularly in conditions in which both TNF and IL-1 play a causative
CC	role. They may be used to treat cachexia, rheumatoid arthritis,
CC	diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
CC	cerebral malaria, allograft and xenograft rejection in graft verses
CC	host disease, sepsis, septic shock, inflammation, allergies and
CC	autoimmune dysfunctions.
XX	
XX	Sequence 1368 BP; 292 A; 424 C; 376 G; 276 T; 0 other;

[illegible]

CC cause a change in the TNFR1 protein. The TNFR1 polymorphisms may be
CC useful for studying the biological function of TNFR1 as well as for
CC identifying drugs targeting the protein for treatment of disorders
CC related to its abnormal expression or function such as tumours,
CC apoptosis related disorders and bacterial infection.
XX
SQ Sequence 1368 bp: 292 A; 424 C; 376 G; 276 T; 0 other;

Query Match	76.3%	Score	651.6;	DB	21;	Length	1368;
Best Local Similarity	95.2%	Pred. No.	3.4e-156;				
Matches	672;	Conservative	34;	Mismatches	0;	Indels	0;
						Gaps	0;

QY	26	atgggctctccaccgtgctgacctgctgctgcgcgcgtggtgctcctgagctgttggtg	85
Db	1	atgggctctccaccgtgctgacctgctgctgcgcgcgtggtcctcctgagctgttggtg	60
QY	86	ggaatataccctcagggttattgactggtgccctcacctagggaacaggagaagaga	145
Db	61	ggaatataccctcagggttattgactggtgccctcacctagggaacaggagaagaga	120
QY	146	gatagtgtgtccccaagaaaatatccaccctcaaaaataattcgatttgcgtgacc	205
Db	121	gatagtgtgtccccaagaaaatatccaccctcaaaaataattcgatttgcgtgacc	180
QY	206	aagtgcacaaaagaaacctacttgtacaatgactgtccaggccggcgaggatcacgac	265
Db	181	aagtgcacaaaagaaacctacttgtacaatgactgtccaggccggcgaggatcacgac	240
QY	266	tgaggaggagtgtagagcggctcttccacggttcagaaaaaacactcaagacactgcctc	325
Db	241	tgaggaggagtgtagagcggctcttccacggttcagaaaaaacactcaagacactgcctc	300
QY	326	agctgctccaaaatgcgcgaagaaaatggctcagggtggagatctcttctgcacagtggac	385
Db	301	agctgctccaaaatgcgcgaagaaaatggctcagggtggagatctcttctgcacagtggac	360
QY	386	cgggacacagctgtgtggctgcaggaagaaccagtacccgattattggagtgaaaacctt	445
Db	361	cgggacacagctgtgtggctgcaggaagaaccagtacccgattattggagtgaaaacctt	420
QY	446	ttccagtgttcaattgcagctcctgcctcctaattggagaccgtgcacctctccttcgcaggag	505
Db	421	ttccagtgttcaattgcagctcctgcctcctaattggagaccgtgcacctctccttcgcaggag	480
QY	506	aaacadaaacacgtgtgcacctgcctcaggtttcttctaaagaaaacacagatgtctc	565
Db	481	aaacadaaacacgtgtgcacctgcctcaggtttcttctaaagaaaacacagatgtctc	540
QY	566	tcctgtagtaactgttaagaaaaccttggagtgcaagaaagtgtgtgcctacccacagattgag	625
Db	541	tcctgtagtaactgttaagaaaaccttggagtgcaagaaagtgtgtgcctacccacagattgag	600
QY	626	aatgtttaaggggcactgaggaactcaggcacccacagtgctgttgcctcgttgcgtccctga	685
Db	601	aatgtttaaggggcactgaggaactcaggcacccacagtgctgttgcctcgttgcgttctctt	660
QY	686	gcctttttcaacagtgcataagcagttttttttgtttttgtttttgttt	731
Db	661	ggctttttgcctttttatccccctctcctcattggttttaattatcctgt	706

RESULT 15
AAT15931
ID AAT15931 standard; DNA: 6889 BP.

XX
XX
XX
DT

DE DHFR/intron (WTrasSD)-TnFr-IgG dicistronic vector.
XX

Recombinant host cell: dihydrofolate reductase: selectable marker:

KW	DHFR; ras splice donor; dicistronic vector; gene expression;
KW	Immunoadhesin; Tnfr-IgG; tumour necrosis factor; ds.
XX	
OS	Synthetic.
XX	
PN	WO9604391-A1.
XX	
PD	15-FEB-1996.
XX	
PF	28-JUL-1995; 95WO-US09576.
XX	
PR	05-AUG-1994; 94US-0286740.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Crowley CW;
XX	
DR	WPI; 1996-129407/13.
XX	
PT	Improved process for the selection of recombinant host cells
PT	expressing high level of a desired product - uses eukaryotic host
PT	cells contg. a DNA construct comprising a selectable gene
XX	
PS	Example 2; Page 36-42; 137pp; English.
XX	
CC	A dicistronic vector (AAT15930) comprises a regulatory region
CC	derived from the cytomegalovirus immediate-early gene, a
CC	selectable dihydrofolate reductase gene positioned within an
CC	intron having a 5' wild-type ras splice donor site, a downstream
CC	sequence coding for an immunoadhesin, Tnfr-IgG, capable of binding
CC	tumour necrosis factor, and a poly-A sequence. Transfection of C
CC	DHFR- cells and subsequent methotrexate amplification and growth
CC	the cells in nutrient-rich medium gave Tnfr-IgG in yields of 9.5
CC	ug/ml (15-fold higher compared to conventional vector amplified
CC	pools).
SQ	Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;

Query Match 76.2%; Score 651; DB 17; Length 6889;
Best Local Similarity 100.0%; Pred. No. 9.1e-156;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	9	ggccaatgactgtctctggcaatggccctctccacacgtgctcaccctgactgtctgctcgcactcgggtgc	68
Db	1588	ggccaatgactgtctctggcaatggccctctccacacgtgctcaccctgactgtctgctcgcactcgggtgc	1647
Qy	69	tccttgagactgtgtgtgggaataataccctcaggggttatattggacttggttcctccacctag	128
Db	1648	tccttgagactgtgtgtgggaataataccctcaggggttatattggacttggttcctccacctag	1707
Qy	129	gggacaggaggagagatagtgtgtgtccccaaggaaaaatatatccaccctcacaata	188
Db	1708	gggacaggaggagagatagtgtgtgtccccaaggaaaaatatatccaccctcacaata	1767
Qy	189	attcgatttgcgtaccaaagtccacaagaagaccttacttgtacaaatgactgtccaggcc	248
Db	1768	attcgatttgcgtaccaaagtccacaagaagaccttacttgtacaaatgactgtccaggcc	1827
Qy	249	cgggcaggatcacgactgcaggagtgtagagcggctccttcacgccttcagaaaaac	308
Db	1828	cgggcaggatcacgactgcaggagtgtagagcggctccttcacgccttcagaaaaac	1887
Qy	309	acctcagacactgctcactgctctccaaatgcggaagaagaaatgggtcaggttgagatct	368
Db	1888	acctcagacactgctcactgctctccaaatgcggaagaagaaatgggtcaggttgagatct	1947
Qy	369	ctctctgcacagtggaccgggacacccgtgtgtggctgcagggaagaccagtaccgcatt	428
Db	1948	ctctctgcacagtggaccgggacacccgtgtgtggctgcagggaagaccagtaccgcatt	2007
Qy	429	attggagtgaacaacattttccagtgcttcaattgcagcctctgcctcaatcgggacogtgc	488
Db	2088	attgaagtgaacaacattttccagtgcttcaattgcagcctctgcctcaatcgggacogtgc	2067

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OM nucleic - nucleic search, using sw model

Run on: August 14, 2001, 05:37:38 ; Search time 80.45 Seconds
(without alignments)
2009.592 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	676.6	79.2	2062	1 US-08-050-319B-24	Sequence 24, Appl
2	676.6	79.2	2062	2 US-08-465-982-24	Sequence 24, Appl
3	676.6	79.2	2161	3 US-09-106-038A-1	Sequence 1, Appl
4	676.6	79.2	2175	1 US-08-321-668-1	Sequence 1, Appl
5	676.6	79.2	2175	1 US-08-837-941-1	Sequence 1, Appl
6	676.6	79.2	2175	1 US-08-126-016-1	Sequence 1, Appl
7	651	76.2	6889	1 US-08-286-740-2	Sequence 2, Appl
8	651	76.2	6889	5 PCT-US95-09576-2	Sequence 2, Appl
9	635.8	74.4	6896	2 US-08-627-151A-6	Sequence 6, Appl
10	595.2	69.7	600	1 US-08-050-319B-47	Sequence 47, Appl
11	595.2	69.7	600	2 US-08-465-982-47	Sequence 47, Appl
12	514	60.2	1301	4 US-08-804-166-7	Sequence 7, Appl
13	514	60.2	1301	4 US-08-910-991-7	Sequence 7, Appl
14	506	59.3	1147	4 US-08-804-166-5	Sequence 5, Appl
15	506	59.3	1147	4 US-08-910-991-5	Sequence 5, Appl
16	503	58.9	504	1 US-08-050-319B-56	Sequence 56, Appl
17	503	58.9	504	2 US-08-465-982-56	Sequence 56, Appl
18	501	58.7	501	1 US-08-050-319B-1	Sequence 1, Appl
19	501	58.7	501	2 US-08-465-982-1	Sequence 1, Appl
20	424.4	49.7	1049	4 US-08-804-166-1	Sequence 1, Appl
21	424.4	49.7	1049	4 US-08-910-991-1	Sequence 1, Appl
22	424.4	49.7	1202	4 US-08-804-166-3	Sequence 3, Appl
23	424.4	49.7	1202	4 US-08-910-991-3	Sequence 3, Appl
24	408.8	47.9	1956	2 US-08-762-308-10	Sequence 10, Appl
25	377.8	44.2	477	1 US-08-050-319B-53	Sequence 53, Appl
26	377.8	44.2	477	1 US-08-465-982-53	Sequence 53, Appl
27	372	43.6	372	1 US-08-050-319B-3	Sequence 3, Appl

28	372	43.6	372	2 US-08-465-982-3	Sequence 3, Appl
29	357.2	41.8	474	1 US-08-050-319B-49	Sequence 49, Appl
30	357.2	41.8	474	1 US-08-465-982-49	Sequence 49, Appl
31	312.4	36.6	462	1 US-08-050-319B-51	Sequence 51, Appl
32	312.4	36.6	462	2 US-08-465-982-51	Sequence 51, Appl
33	39.4	4.6	665	1 US-08-322-742-17	Sequence 17, Appl
34	39.2	4.6	1737	1 US-08-202-056-4	Sequence 4, Appl
35	39.2	4.6	1737	1 US-08-076-093A-3	Sequence 3, Appl
36	39.2	4.6	1737	1 US-08-701-265-3	Sequence 3, Appl
37	39.2	4.6	1737	2 US-08-284-586-3	Sequence 3, Appl
38	39.2	4.6	1737	2 US-08-805-478-3	Sequence 3, Appl
39	39.2	4.6	1737	2 US-08-802-627A-3	Sequence 3, Appl
40	39.2	4.6	1737	2 US-08-801-238-3	Sequence 3, Appl
41	39.2	4.6	1737	2 US-08-801-228-3	Sequence 3, Appl
42	39.2	4.6	1737	3 US-09-104-296-3	Sequence 3, Appl
43	39.2	4.6	1737	5 PCT-US94-06380-2	Sequence 2, Appl
44	39	4.6	246240	2 US-08-724-394A-20	Sequence 20, Appl
45	39	4.6	246240	2 US-08-724-394A-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-050-319B-24
; Sequence 24, Application US/08050319B
; Patent No. 5633145
; GENERAL INFORMATION:
; APPLICANT: M.Feldmann, P.W. Gray,
; APPLICANT: M.J.C. Turner, F.M Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,319B
; FILING DATE: 10-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2062 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 155..1519
; US-08-050-319B-24

Query Match 79.2%; Score 676.6; DB 1; Length 2062;
Best Local Similarity 95.3%; Pred. No. 8.4e-187;
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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QY 1 gaggagagccatagctgtctggcagtgagcctctccacagtgccctgacccgtgctgtgccc 60
Db 130 GAGTGAGAGGCCATAGCTGTGTGGCATGGCCCTCTCCACCGTGCCTGACCTGTGCTGCC 189
QY 61 gctgggctcctgagctgtgtggaatataccctcaggggttatgtgactggtgcc 120
Db 190 GCTGGTGTCTCTGGAGCTGTGTGGGAATATACCCCTCAGGGGTATTGGACTGGTCCC 249
QY 121 tcaactaggggagcaggagagagatagctgtgtgtccccaaggaaatatatccaccc 180
Db 250 TCACCTAGGGACAGGAGAGAGATAGTGTGTCTCCCAAGGAATAATATCCACCC 309
QY 181 tcaataatctgattgtgtgtaccagtgcccaaggaaacctactgttacaatgactg 240
Db 310 TCAATAATATTCGATTGTGTGTACCAAGTCCCAAGGAACCTACTGTGTACAAATGACTG 369
QY 241 tccagcccgggcagagatagcagctcagggagtgagagcgtctcctccacgcttc 300
Db 370 TCAGAGCCCGGGCAGGATACGACTGCAGGGAGTGTGAGAGCGGCTCTTCACCGCTTC 429
QY 301 agaaaaccacctcagacactgctcagctgtcctcaaatgccaatgagcctcctcaatgg 360
Db 430 AGAAACCACCTCAGACACTGCCTCAGCTGTCCAATGCGAAAGGAATGGTCAAGT 489
QY 361 ggagatctcttctgacagtgaccgggagccogtgtgtggtgcagggaaccagta 420
Db 490 GGAGATCTCTTCTTGACACTGGACCGGACACCGTGTGTGGCTGCAGGAAGAACCACTA 549
QY 421 ccggcattattgagtgaaaccttttccagtgcttcaatgtcagcctctgacctgaggtt 540
Db 550 CCGGCATATTGGAGTGAAACCTTTTCCAGTGCTTCAATGTCAGCGCTCTGCCCTCAATGG 609
QY 481 gacgtgcacctctcctgcagagagaaacagacacccgtgtgcaacctgccaatgaggtt 540
Db 610 GACCGTGCACTCTCTCTGCAGAGAAACAGACACCGTGTGCACCTGCCATGCGAGGTTT 669
QY 541 ctttctaagagaaacagtgctgtcctctgtagtaactgaagaaagcctggagtgac 600
Db 670 CTTTCTAAGAGAAACAGTGCTGTCTCTGTAGTAAGTGTAAAGAAAGCGCTGGAGTGCAC 729
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Db 730 GAAGTTGTGCTCTACCCAGATTGAGAAATGTTAAGGGCACTGAGGCACTCAGGCACCACT 789
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QY 721 ttgtttttgtt 731
Db 850 AATGATATCGCT 860
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RESULT 2
US-08-465-982-24
; Sequence 24, Application US/08465982
; Patent No. 5863786
; GENERAL INFORMATION:
; APPLICANT: M.Feldmann, P.W. Gray,
; APPLICANT: M.J.C. Turner, F.M. Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,982
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,319
; FILING DATE: 10-May-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2062 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 155..1519
; US-08-465-982-24
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Query Match 79.2%; Score 676.6; DB 2; Length 2062;
Best Local Similarity 95.3%; Pred. No. 8.4e-187;
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 gaggagagccatagctgtgtggaatataccctcaggggttatgtgactggtgcc 60
Db 130 GAGTGAGAGGCCATAGCTGTGTGGCATGGCCCTCTCCACCGTGCCTGACCTGTGCTGCC 189
QY 61 gctgggctcctgagctgtgtggaatataccctcaggggttatgtgactggtgcc 120
Db 190 GCTGGTGTCTCTGGAGCTGTGTGGGAATATACCCCTCAGGGGTATTGGACTGGTCCC 249
QY 121 tcaactaggggagcaggagagagatagctgtgtgtccccaaggaaatatatccaccc 180
Db 250 TCACCTAGGGACAGGAGAGAGATAGTGTGTCTCCCAAGGAATAATATCCACCC 309
QY 181 tcaataatctgattgtgtaccagtgcccaaggaaacctactgttacaatgactg 240
Db 310 TCAATAATATTCGATTGTGTGTACCAAGTGCACAGGAGTGTGTGGCTGCAGGAAGAACCACTA 369
QY 241 tccagcccgggcagagatagcagctcagggagtgagagcgtctcctccacgcttc 300
Db 370 TCAGAGCCCGGGCAGGATACGACTGCAGGGAGTGTGAGAGCGGCTCTTCACCGCTTC 429
QY 301 agaaaaccacctcagacactgctcagctgtcctcaaatgccaatgagcctcctcaatgg 360
Db 430 AGAAACCACCTCAGACACTGCCTCAGCTGTCCAATGCGAAAGGAATGGTCAAGT 489
QY 361 ggagatctcttctgacagtgaccgggagccogtgtgtggtgcagggaaccagta 420
Db 490 GGAGATCTCTTCTTGACACTGGACCGGACACCGTGTGTGGCTGCAGGAAGAACCACTA 549
QY 421 ccggcattattgagtgaaaccttttccagtgcttcaatgtcagcctctgacctgaggtt 480
Db 550 CCGGCATATTGGAGTGAAACCTTTTCCAGTGCTTCAATGTCAGCGCTCTGCCCTCAATGG 609
QY 481 gacgtgcacctctcctgcagagagaaacagacacccgtgtgcaacctgccaatgaggtt 540
Db 610 GACCGTGCACTCTCTCTGCAGAGAAACAGACACCGTGTGCACCTGCCATGCGAGGTTT 669
QY 541 ctttctaagagaaacagtgctgtcctctgtagtaactgaagaaagcctggagtgac 600
Db 670 CTTTCTAAGAGAAACAGTGCTGTCTCTGTAGTAAGTGTAAAGAAAGCGCTGGAGTGCAC 729
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QY 601 gaagttgtcctaccacagattgagaattgttaaggccactgaggactcaggcaccacaggt 660
Db 730 GAAGTTGTGCTACCCACAGATGAGAATGTTAAGGGCACTGAGGACTCAGGCACACAGT 789
QY 661 gctgtgcccctgttgcctcagcagctttttcacagtgcatagcaggtttttttgtt 720
Db 790 GCTGTGCCCCGTGTCATTTCTTGTGCTTGTGCTTTTATCCCTCTTCATTTGGTTT 849
QY 721 ttgtttttgtt 731
Db 850 AATGATATCGCT 860
RESULT 3
US-09-106-038A-1
; Sequence 1, Application US/09106038A
; Patent No. 6007995
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker and Lex M. Cowseert
; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFRI
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Isis Pharmaceuticals, Inc.
; STREET: 2292 Faraday Avenue
; CITY: Carlsbad
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92008
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,038A
; FILING DATE: June 26, 1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Laurel Spear Bernstein
; REGISTRATION NUMBER: 37,280
; REFERENCE/DOCKET NUMBER: RTS-0004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (760) 931-9200
; TELEFAX: (760) 603-3820
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-106-038A-1
Query Match 79.2%; Score 676.6; DB 3; Length 2161;
Best Local Similarity 95.3%; Pred. No. 8.6e-187;
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 1 gagtggagggccatagctgtgtgcatgggctctccaccgtgctgacctgctgctgctgcc 60
Db 231 GAGTGAGAGGGCCATAGCTGTGTCGATGGGCTCTCCACCGCTGCTGACCTGCTGCTGCC 290
QY 61 gctgtgtcctcagcagctgtgtgtggaataaccctcaggggttatggactggtccc 120
Db 291 GCTGTGCTCCTGGAGCTGTTGTTGGGAATATACCCCTCAGGGGTTATTGGAGTGTGCC 350
QY 121 tcacctaggggacaggagagaagatagtggtgtccccaagaaaaatatatccacc 180
Db 351 TCACCTAGGGGACAGGAGAGAGATAGTGTGTGTGTCGCCCAAGAAAAATATATCCACCC 410
QY 181 tcaaaataatcgtattgtgtgtacaaagtcacaaaggaacacctactgtacaatgactg 240
Db 411 TCAAAATAATTCGATTGCTGTACCAAGTGCACAAAGGAACCTACTGTGTACATGACTG 470

QY 241 tccagggccggggcaggatatacggactgaggagtgagagcggctccttaccgccttc 300
Db 471 TCCAGGCCCCGGGCGCAGGATACGACTGCAGGGAGTGTGAGAGCGGCTCCTTCAACGCGTTC 530
QY 301 aaaaaaacaccctcagacactgctcagctgctccaaatgccgaagaaaatgggtcaggt 360
Db 531 AGAAAACACCCTCAGACACTGCCTCAGCTGCTCCAATGCCGAAGAAAATGGGTGAGGT 590
QY 361 ggagatctctcttgcacagtggaacggggacacccgtgtgtggctgagggaagaccagta 420
Db 591 GGAGATCTCTTCTTGACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACAGTA 650
QY 421 ccggcattatggagtgaaaaccttttccagtgcttcaattgcagcctctgcctcaatgg 480
Db 651 CCGGCATTATTGGAGTGAACACCTTTTCCAGTGTCTCAATTGCGAGCTCTGCTCAATGG 710
QY 481 gaccgtgacctctcctgccaggagaaaacagaaacacccgtgtgcacctgcaatcaggttt 540
Db 711 GACCGTGACCTCTCTCTGCCAGGAAACAGAACACCGTGTGCACCTGCCATGCAGGTTT 770
QY 541 ctttctaagagaaaacgagtgctgtctcctgtagtaactgaaagaaagcctggagtgac 600
Db 771 CTTTCTAAGAGAAACGAGTGTGTCTCTCTGTAGTAACTGTAAAGAAAGCCTGGAGTGCAC 830
QY 601 gaagttgtcctaccacagattgagaattgttaaggccactgaggactcaggcaccacag 660
Db 831 GAAGTTGTGCTACCCACAGATTGAGAAATGTTAAGGGCACTGAGGACTCAGGCACACAGT 890
QY 661 gctgtgtcccctggttgcctgagcctttttcacagtgcatagcaggtttttttgtt 720
Db 891 GCTGTGCCCCGTGTCATTTCTTGTGCTTGTGCTTTTATCCCTCTCTCTCTCTCTCTT 950
QY 721 ttgtttttgtt 731
Db 951 AATGATATCGCT 961
RESULT 4
US-08-321-668-1
; Sequence 1, Application US/08321668
; Patent No. 5665859
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; APPLICANT: VARFOLOMEEV, Eugene
; APPLICANT: BATKIN, Michael
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/321,668
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107268
; FILING DATE: 12-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-13

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2175 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 256..1620

US-08-321-668-1

Query Match 79.2%; Score 676.6; DB 1; Length 2175;

Best Local Similarity 95.3%; Pred. No. 8.6e-187;

Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 1 gactgagagccatagctgtcgtgcatggccctccacccgtacccctgacctgctgctgcc 60

Db 231 GAGTGAGAGCCATAGCTGCTGGCATGGCCCTCTCCACCGTGGCTGACCTGCTGCTGCC 290

Qy 61 gctggtgctcctgagctgtgttgggaatataccctcaggggttattggactggtccc 120

Db 291 GCTGGTGTCTCTGAGCTGTGGTGGGAATATACCCCTCAGGGGTATTGGACTGGTCCC 350

Qy 121 tcacctaggggacagggagagagatagtggtgtgtccccaaggaaatatatccaccc 180

Db 351 TCACCTAGGGGACAGGAGAGAGATAGTGTGTCTCCCAAGGAAATATATCCACCC 410

Qy 181 tcaaaataattcattgtgtaccaggtcccaaggtcccaaggaactactgtacaatgactg 240

Db 411 TCAAAATAATTCTGCTGTACCAAGTGCCCAAGGAACCTTGTGTACAATGACTG 470

Qy 241 tcaggccggggcaggatagcagactgagggagtgagagcggtccttcacccgttc 300

Db 471 TCCAGGCCGGGCGAGATACGGACTCAGGAGTGTGAGAGCGGCTCCTTCACCGCTTC 530

Qy 301 agaaaccacctcagacactgctcagctgctcacaatgccgaagaaatgggtcaggt 360

Db 531 AGAAACCACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAGAAATGGGTCAAGT 590

Qy 361 gtagatctcttgcacagtggaccgggacacgtgtgtgtgtgtgtgtgtgtgtgtgtgt 420

Db 591 GGAGATCTCTCTTGCACAGTGGACCGGGGACACCGTGTGTGGTGTGCGAGGAAGAACAGTA 650

Qy 421 ccggcattattgagtgaaacacctttccagtgcttcaattgagcgtctgctcactgg 480

Db 651 CCGGCATTATTGGAGTGAAACCTTTCCAGTGTCTCAATTGACGCTCTGCCCTCAATGG 710

Qy 481 gaccgtgacctctctgccagagagaacacacacgtgtgacacctgacctgacctgttt 540

Db 711 GACCGTGACCTCTCTCGCAGGAGAAACACACACCGTGTGACCTGCGCATGCAAGTTT 770

Qy 541 ctttctaaggaagaaacagtggtgtcctctgttagtaactgtaagaaagcctggagtgac 600

Db 771 CTTTCTAAGAGAAACAGAGTGTGTCTCTGTAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 830

Qy 601 gaagtgtgctcctccacagattgagaatgttaaggccacgtgagacactcagaccacagt 660

Db 831 GAAGTGTGCTCTACCCAGATTGAGAAATGTTAAGGGGACCTGAGGACCTCAGGACCAAGT 890

Qy 661 gctgtgcccctgttgcctgcccctgagcctttttcacagtgatgataagcagttttttgtt 720

Db 891 GCNGTGGCCCTGGTCATTTCTTGGTCTCTTATCCCTTCTCTCTCTCTCTCTCTCTCTCT 950

Qy 721 ttgtttttgtt 731

Db 951 AATGTATCGCT 961.

RESULT 5

US-08-837-941-1

; Sequence 1, Application US/08837941

; Patent No. 5766917

; GENERAL INFORMATION:

; APPLICANT: WALLACH, David

; APPLICANT: BRAKEBUSCH, Cord

; APPLICANT: VARFOLOMEEV, Eugene

; APPLICANT: BATKIN, Michael

; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF

; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/837,941

; FILING DATE: 28-APR-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/321,668

; FILING DATE: 12-OCT-1994

; APPLICATION NUMBER: IL 107268

; FILING DATE: 12-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: BROWDY, Roger L.

; REGISTRATION NUMBER: 25,618

; REFERENCE/DOCKET NUMBER: WALLACH-13

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; TELEX: 248633

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2175 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 256..1620

; US-08-837-941-1

Query Match 79.2%; Score 676.6; DB 1; Length 2175;

Best Local Similarity 95.3%; Pred. No. 8.6e-187;

Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 1 gactgagagccatagctgtcgtgcatggccctccacccgtacccctgacctgctgctgcc 60

Db 231 GAGTGAGAGCCATAGCTGCTGGCATGGCCCTCTCCACCGTGGCTGACCTGCTGCTGCC 290

Qy 61 gctggtgctcctgagctgttgggaatataccctcaggggttattggactggtccc 120

Db 291 GCTGGTGTCTCTGAGCTGTGGTGGGAATATACCCCTCAGGGGTATTGGACTGGTCCC 350

Qy 121 tcacctaggggacagggagagagatagtggtgtgtccccaaggaaatatatccaccc 180

Db 351 TCACCTAGGGGACAGGAGAGAGATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 410

Qy 181 tcaaaataattcattgtgttaccaggtgcccaaggaacactactgtacaatgactg 240

Db	411	TCAAAATAATTCAATTTGCTGTACCAAGTGCACCAAAAGGAACCTACTTGTCAATGACTG	470
QY	241	tccaggccggcgagagatacgaactgcgaggagtgtagagcggctccttcacgcgttc	300
Db	471	TCCAGGCCGGGCGAGATACGACTGCAGGGAGTGTGAGAGCGGCTCTTCACCGCTTC	530
QY	301	agaaaccacctcagacactgctcctcagctgctccaaatgccgaaggaataatgggtcaggt	360
Db	531	AGAAAACCACTCAGACACTGCCTCAGCTGCTCCAAATGCCAAAAGGAAATGGTCAAGT	590
QY	361	ggagatctctctgcacagtggacagggaacacctgctggtgcgagaaagaaccagta	420
Db	591	GGAGATCTCTTCTTGACACTGACCGGACACCGTGTGTGGCTGCAGGAAGAACCACTA	650
QY	421	ccggcattatggagtgaaaacctttccagtgctccaattgcagcctctgctcaatgg	480
Db	651	CCGGCATATTGGAGTGAAACCTTTTCAGTGTCTCAATTGCAGCCTCTGGCTCAATGG	710
QY	481	gacctgcacctctctgcaggagaaaaacagaaacacctgtgcactgccaatgcaggttt	540
Db	711	GACCGTGCACCTCTCTCGCAGGAGAAACAGAACACCGTGTGCACCTGCATGCAGGTTT	770
QY	541	ctttctaagaaaaaacgagtgtctctctgtagtaactgaagaaagcctggagtgcaac	600
Db	771	CTTTCTAAGAGAAAACGAGTGTCTCTCTGTAGTAAGTCTAAGAAAAGCCTGGAGTGCA	830
QY	601	gaagtgtgctaccaccagattgagaatgttaaggcactgaggaactcaggcaccacagt	660
Db	831	GAAGTTGTGCTTACCCAGATTGAGAAATGTTAAGGCACCTGAGGACTCAGGCACCACAGT	890
QY	661	gctgtgtccctggttcgtccctcagcctcttttcacagtgcataagcagttttttttgtt	720
Db	891	GCCTGTGGCCCTGGTCATTTCCTTTGGCTCTTTGGCTTTATCCCTCCTCTTCATGGTTT	950
QY	721	tttgtttttgtt	731
Db	951	AATGTATCGCT	961

RESULT 6

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US-08-126-016-1
; Sequence 1, Application US/08126016
; Patent No. 5811261
; GENERAL INFORMATION:
; APPLICANT: WALLACH, DAVID
; APPLICANT: NOPHAR, YARON
; APPLICANT: KEMPER, OLIVER
; APPLICANT: ENGELMANN, HARTMUT
; APPLICANT: BRAKEBUSCH, CORD
; APPLICANT: ADERKA, DAN
; TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/126,016
; FILING DATE: 24-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/625568
; FILING DATE: 13-DEC-1990
; ATTORNEY/AGENT INFORMATION:

```

```

NAME: BROWDY, ROGER L
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 256..1620
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 319..1620
US-08-126-016-1

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Query Match	79.2%;	Score 676.6;	DB 1;	Length 2175;
Best Local Similarity	95.3%;	Pred. No. 8.6e-187;		
Matches 697:	Conservative	0;	Mismatches 34;	Indels 0;
	Gaps			

Qy	1	gagtagaggccatagctgtctggca	tgggcctctccaccgctgacctgtctgtgc	60
Db	231	GAGTGAGAGGCCATAGCTGTG	CATGGCCCTTCACACGTCGCTGACCTGCTGTGTGC	230
Qy	61	qctggtcctctgagcgtgtgtgg	aaatataccctcagggttatgtgactgtccc	120
Db	291	GCTGGTGCTCTGAGCTGTGG	TGGGAATATACCCCTCAGGGGTATTGGACTGTGTCC	350
Qy	121	tcacctagggcaggagagagata	gtgtgtgtccccaaggaaaaatatccaccc	180
Db	351	TCACCTAGGGACAGGAGAGAG	ACTGTGTGTCCCAAGGAAATATATCCACCC	410
Qy	181	tcaaaataattcgtattgctgt	taccaaagtgccaaaggaaacbtacttgtacaatgactg	240
Db	411	TCAAAATAATTCGATTTCGT	TACCAAGTGCCCAAGGAACCTACTGTGTACAAATGACTG	470
Qy	241	tccaggccgggcagatcacgact	caggaqtccaggagtgagagcgctccttcaccgcttc	300
Db	471	TCCAGGCCCGGGCAGGATAC	GGACTCAGGGAGTGTGAGAGCGCTCTCTTACCCGCTTC	530
Qy	301	agaaaccactcagacactgcct	cagctgcctccaaatgccgaaaggaaatgggtcaggt	360
Db	531	AGAAACCACCTCAGACACTG	CGCTCAGCTGCTCCAAATGCCGAAGGAATGGGTGAGGT	590
Qy	361	ggagatctctcttgacagtgac	agcgggacaccggtgtgtgctgcaggagaagaccagta	420
Db	591	GGAGATCTCTTTTCACAGT	TGACCGGGACACCGTGTGTGGCTGCAGGAAGAACAGTA	650
Qy	421	ccgscattatggagtgaaacct	tttccagtgcttcaattgcagcctctgcctcaatgg	480
Db	651	CCGSCATTATGGAGTCGAA	AAACCTTTTCCAGTGTCAATTGGCAGCCTCTGCCCTCAATGG	710
Qy	481	gaccgtgcactctctgcgagag	aaacacacggtgtgcacctgccatgcaggttt	540
Db	711	GACCGTGCACTCTCTCTG	CAGGAGAAACAGACACCGTGTGCACCTGCCATGCAGGTTT	770
Qy	541	ctttctaaggagaacacagtg	tgtctctctgtagtaactgtaaagaagcctggagtgac	600
Db	771	CTTTCTAAGAGAAACAGAG	TGTGTCTCCTGTAGTAACTGTGAAGAAAGCCTGGAGTGCAC	830
Qy	601	gaagtgtgctaccaccagatt	gaagaatgtaaagggcactgaggaactcaggaccacagt	660
Db	831	GAAGTGTGCTCTACCCCA	GATTGAGAAATGTTAAGGGCACTTGAGACTTCAGGCACACAGT	890
Qy	661	gctgtgcccctggtctgctcc	tgagccttttcacagtgcataagcagttttttttgtt	720


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Best Local Similarity 100.0%; Pred. No. 4.4e-179;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ggcataagctgtcgtgcatggcctcctccacgctcctgacgtgtgctgcgctgggtgc 68
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QY 69 tcttgagctgttgggtggaataataaccctcaggggttattggactgtccctcacctag 128
Db 1648 TCCTGGAGCTGTGTGGGAATATACCCCTCAGGGGTTATTGGAGTGTCCCTCACCTAG 1707

QY 129 gggcagggagagagagatagtgtgtgtccccaaggagaaatatatccacctcaaaata 188
Db 1708 GGGACAGGAGAGAGATAGTGTGTCTCCCAAGGAAATATATCCACCTCAAAATA 1767

QY 189 attgattgtgtaccagtgccacaagaactacttataatgactgtccagacc 248
Db 1768 ATTGATTGTGTACCAAGTGCCACAAGGAACCTACTTGTACAAATGACTGTCCAGGCC 1827

QY 249 cggggcagatcacgactgcaggagtgtagagcggctcctccaccgttcagaaaacc 308
Db 1828 CGGGCAGGATACGAGCTGCAGGGAGTGTGAGCGGCTCTTCACCGTTCAGAAACC 1887

QY 309 acctcagacactgctcagctgtctccaaatgccgaagaaatgggtcaggtggagatct 368
Db 1888 ACCTCAGACACTGCTCAGCTGTCTCAAAATGCCAAGAAATGGGTGAGATCT 1947

QY 369 cttcttgacagtgagcggagacacgctgtgtgctgcaggagaacacagtaaccggaatt 428
Db 1948 CTTCTTGACAGTGGACCGGACACCGGTGTGGCTGCAGGAAGAACAGTACCGGCATT 2007

QY 429 attgagtgaaaacctttccagtgcttcaattgcagcctctgcctcaatgggacgtgc 488
Db 2008 ATTGGAGTGAACCTTTTCAGTGCTTCAATTGGAGCCTCTGCCTCAATGGGACCGTGC 2067

QY 489 acctctctgcagagagagaaacagacacccgtgtgcacctgcacatgcaggtttcttctaa 548
Db 2068 ACCTCTCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCATGCAGGTTCCTTTCTAA 2127

QY 549 gagaaaacagtgctgtctcctgtagtaactgtaaagaaagcctgagtgacagagtgct 608
Db 2128 GAGAAAACAGTGCTGTCTCTGTAGTACTGTAAAGAAAGCGCTGGAGTGCAGGAAGTGT 2187

QY 609 gcctaccacagatgagaatttaaggacactgaggaactcaggaaccacag 659
Db 2188 GCCTACCCAGATTGAGAAATGTTAAGGGCACTGAGGACTCAGGCACACAG 2238

RESULT 9
US-08-627-151A-6
; Sequence 6, Application US/08627151A
; Patent No. 5866341
; GENERAL INFORMATION:
; APPLICANT: SPINELLA, Dominic
; APPLICANT: BECHERER, Kathleen
; APPLICANT: BROWN, Steven
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; SCREENING DRUG LIBRARIES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gen-Probe Incorporated
; STREET: 10210 Genetic Center Drive
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,151A
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; FILING DATE: 03-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fisher, Carlos A
; REGISTRATION NUMBER: 36,510
; REFERENCE/DOCKET NUMBER: CB1016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-410-8926
; TELEFAX: 619-410-8928
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6896 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-627-151A-6

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Best Local Similarity 98.9%; Pred. No. 1.1e-174;
Matches 640; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 75 agctgtgtggggaataataccctcaggggttattggactgttccctcacctcaggggaca 134
Db 984 AGCTGTGTGGGAATATACCCCTCAGGGGTTATTGGACTGTGCTCCTCCTCAGTAGG 1043

QY 135 gggagaagagagatagtgtgtgtccccaaggagaaatatatccacctcaaaaataattcga 194
Db 1044 GGGAGAAGAGAGATAGTGTGTGTCCCAAGGAAATATATCCACCTCAAAATAATTGCA 1103

QY 195 ttgtgtgtaccagtgccaaaagaaacactactgttacaatgactgtccagggccggggc 254
Db 1104 TTTGTGTGTACCAAGTCCCAAGGAACCTACTTGTACAAATGACTGTCCAGGCGCGGG 1163

QY 255 aggatacagactgcaggaggtgtgagagcggtcctcctcaccgttccagaaacacacctca 314
Db 1164 AGGATACGAGACTGCAGGAGTGTGAGAGCGGCTCTTCCACCGTTTCAGAAAACACCTCA 1223

QY 315 gacactgcctcagctgtcctcaaatgccaaagaaatgggtcaggtggagatctcttctt 374
Db 1224 GACACTGCCTCAGCTGCTCCAAATGCCAAAGGAAATGGGTGAGTGAGATCTCTTCTT 1283

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QY 495 cctgcagagagaaacagacacccgtgtgcacctgcacatgcacgtgttcttcttaagagaaa 554
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QY 555 acgagtgtctcctgttagtaactgttaaaaaagcctgcaggtgcacgaagtgtgcttac 614
Db 1464 ACGAGTGTCTCTCTGTAGTACTGTAAAGAAAGCGCTGGAGTGCAGGAGTGTGCTGCTAC 1523

QY 615 ccagattgagaattttaaggacactgaggaactcaggaaccacagtg 661
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RESULT 10
US-08-050-319B-47
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; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1301 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 279..1287
; US-08-804-166-7

Query Match          60.2%; Score 514; DB 4; Length 1301;
Best Local Similarity 100.0%; Pred. No. 1e-139;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 146 gatagtggtgtgtcccaaggaataatatccaccctcaaaataatctgattgctgtacc 205
Db 345 GATAGTGTGTGTCCTCCCAAGGAATAATATCCACCCTCAAAATAATTCGATTGCTGTACC 404
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Db 705 AAACAGAACACCGGTGCACTGCCATGCAAGTTCTTTCTTAAGAGAAACAGAGTGTGTC 764
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RESULT 13
US-08-910-991-7
; Sequence 7, Application US/08910991
; Patent No. 6194177
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappell, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W.,
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:

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Db 584 CGGGACACCGTGTGGTGTGAGGAGAACACAGTACCGGCATTATTGGAGTGAACACCTT 643
QY 446 tccagtgcttcaattgacgctctgctcaatgggacgctgacacctctcctgccaaggag 505
Db 644 TTCAGTGTCTCAATTGACCTCTGCTCTCAATGGACCGTGCACCTCTCCCTGTCAGGAG 703
QY 506 aaacagaacacgctgtgacacgtgacacgtgacacgtgacacgtgacacgtgacacgtgac 565
Db 704 AAACAGAACACCGTGTGACCTGTGACCTGTGACCTGTGACCTGTGACCTGTGACCTGTG 763
QY 566 tccctagtagtaactgaagaaacgctgagtgacgagtgacgagtgacgagtgacgagtgac 625
Db 764 TCCTGTAGTAACTGAAGAAAGCCTGGAGTGCACGAAGTGTGCTCCCTACCCACAGATTGAG 823
QY 626 aatgtaaggacgactgagacgactgagcaccacag 659
Db 824 AATGTTAAGGGCACTGAGGACTCAGGCACACAG 857

RESULT 15

US-08-910-991-5
; Sequence 5, Application US/08910991
; Patent No. 6194177
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,991
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/804,166
; FILING DATE: 20 February 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/011,936
; FILING DATE: 20 February 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: CAMPBELL-2B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1147 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 278..1132
US-08-910-991-5

Query Match 59.3%; Score 506; DB 4; Length 1147;

Best Local Similarity 99.0%; Pred. No. 2e-137;
Matches 509; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 146 gatagtggtgtcccaagaaataatccaccctcaaaataattcgattgtctgtacc 205
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QY 206 aagtgcacaaaagaaacctactgtacaatgactgtccagcccggggagagatacggac 265
Db 404 AAGTGCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGCGCAGATACCGAC 463
QY 266 tgaggagtgtagagcggctccttcacgcgttcagaacacacacacacacacacacac 325
Db 464 TGCAGGAGTGTGAGAGCGGCTCTTCACCGCTTCAGAAAAACACCTCAGACACTGCCTC 523
QY 326 agtgtgtccaaatgccgaagaaatgggtcagtgagatctcttcttcacagtgac 385
Db 524 AGTGTCTCCAAATGCCGAAAGAAATGGGTGAGGATCTCTTCTGTGCACAGTGGAC 583
QY 386 cgggacacccgtgtgtgctgcaggaagaaccagTaccggcattattggagtgaacacct 445
Db 584 CGGACACCGTGTGTGCTGCAGGAAGAACAGTACCGGCATTATTGGAGTGAAACCTT 643
QY 446 tccagtgcttcaattgacgctcctgcctcaatgggacgctgacacctctcctgccaaggag 505
Db 644 TTCAGTGTCTCAATTGACCTCTGCTCTCAATGGACCGTGCACCTCTCCTGTCCAGGAG 703
QY 506 aaacagaacacgctgtgacacgtgacacgtgacacgtgacacgtgacacgtgacacgtgac 565
Db 704 AAACAGAACACCGTGTGACCTGTGACCTGTGACCTGTGACCTGTGACCTGTGACCTGTG 763
QY 566 tccctagtagtaactgaagaaacgctgagtgacgagtgacgagtgacgagtgacgagtgac 625
Db 764 TCCTGTAGTAACTGAAGAAAGCCTGGAGTGCACGAAGTGTGCTCCCTACCCACAGATTGAG 823
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Db 824 AATGTTAAGGGCACTGAGGACTCAGGCACACAG 857

Search completed: August 14, 2001, 06:20:01
Job time: 2543 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 14, 2001, 05:36:43 ; Search time 1170.31 Seconds
(without alignments)
6897.947 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 20456230

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

[illegible]

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enriched double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSport 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com
222 a 262 c 252 g 220 t 1 others
BASE COUNT

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Query Match	79.0%	Score 675;	DB 106;	Length 957;
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DB	348	TCAAAATAATTTCGATTGTCTACCAAGTCCCAACGAAGAACCTACTTGTACAAATGACTG	407
QY	241	tcagggccggggcaggatacaggactgcagggaagtgtgagagcggtccttcacgcgttc	300
DB	408	TCAGGCGCGGGCAGGATACGGACTGCAAGGAGTGTGAGCGGCTCTCTCACCGCTTC	467
QY	301	agaaaaccacctcagacactgcctcagctgctccaaatgccgaaggaaatgggtcaggt	360
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ALIGNMENTS

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LOCUS	AL559050
DEFINITION	AL559050 LTI_NFL008.rc2 prime, mRNA sequence.
ACCESSTION	AL559050
VERSION	AL559050.1
KEYWORDS	GI:12904166
SOURCE	EST. human.

ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 957)
AUTHORS	Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	Contact: Genoscope


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BP 191 91006 EVRY cedex - France
Email: segr@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
231 a 258 c 259 g 221 t 6 others
BASE COUNT
ORIGIN

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BASE COUNT 231 a 258 c 259 g 221 t 6 others
ORIGIN

Query Match	77.2%;	Score 659;	DB 106;	Length 975;
Best Local Similarity	97.4%;	Pred. No. 8.7e-167;		
Matches 677; Conservative		3; Mismatches 14;	Indels 1;	Gaps 1;

Qy	1	gagtgagaggccatagctgtctgcatggtggcctctccacogtgcctgacctgctgctgccc	60
Db	231	GAGTGAGAGGCCATAGCTGTCTGGCATGGGGCTCTCCACCGTGCCTGACCTGCCTGCTGCC	290
Qy	61	gctggtcctcctgagctgttggtggaaatataccctcaggggattatggactggctccc	120
Db	291	ACTGGTGCTCTCGAGCTGTGGTGGGAATATACCCCTCAGGGGTATTGTGACTGGTGCTCC	350
Qy	121	tcaactagggaagggagagaagagatagtggtgtgtccccaaggaataatatccacccc	180
Db	351	TCACCTAGGGGACAGGAGAGACAGATAGTGTGTCTCCCAAGGAAATATATCCACCC	410
Qy	181	tcaaaataatcgattgtgtgtaccaggtgccacaaaggaaacctacttgtacaatgactg	240
Db	411	TCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTTACTTGTACAATGACTG	470
Qy	241	tceaggcccgggcagatcacgactcaggggagtgtgaagcgcctcttcacgccttc	300
Db	471	TCCAGGCCCGGGCAGGATACGGACTCGAGGGAGTGTGAGAGCGGCTCTCTTCCCGCTTC	530
Qy	301	agaaacacacctcagacactcctcagctgctccaaatgccgaaggaataatgggtcaggt	360
Db	531	AGAAACACACTCAGACACTGCCTTCAGCTCTCCAATGCCGAAAGGAATGGGTGAGGT	590
Qy	361	ggagatctctcttgcacagtggaacgggacacogtgtgtggtgcagggaagaaccagta	420
Db	591	GGAGATCTCTTCTTGCACAGTGGAGCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTA	650
Qy	421	ccgcattatggagtgaacacctttccagtgttcaattgcagcctctgcctccaatgg	480
Db	651	CCGCATTATTGGAGTGAATAACCTTTCCAGTGTCTCAATTGACAGCCTCTGCCCTCAATGG	710
Qy	481	gaccgtgcacctctcttgcaggaggaacagaacacogtgtgcacctgtgcaatgcaggttt	540
Db	711	GACCGTGACCTCTCTTGCAGGAGGAACAGAACACCGTGTGCCCTGCCATGCAGTTTT	770
Qy	541	cttctcaagagaagaacagagtgtgtctcctgtagttaactgtaaagaaagcctgagtgcaac	600
Db	771	CTTTCTAAGAGAAACAGTGTGTCTCTGTGTAGTAACTGTDAGAAAAGCCCTGGAGTGAC	830
Qy	601	gaagtgtgctaccaccagattgagaatgttaaggggcaactgaggaactcaggcaccacag	659
Db	831	GAAGTGTGTGCTTACCCAGATTCAGAAATGTTAAGGGCACTTCAGGACTCAGGCACCAWAG	890
Qy	660	tgtctgtgccctggtgtcctccctgagcccttttc	694

Query Match	77.3%;	Score 660;	DB 108;	Length 761;
Best Local Similarity	98.1%;	Pred. No. 4.4e-167;		
Matches 666;	Conservative	0;	Mismatches 13;	Indels 0; Gaps
Qy	1	gaqtgagaggccatagctgctcgacatggcgctctccacgctgcctgacactgctgctgc	60	
Db	37	GAGTGAGAGGCCATAGCTGCTGGCATGGGCCCTCCACGTCGCCGACCTGCTGCTGCC	96	
Qy	61	gctggtgctcctgagcgtgtgttgggaatataccctcaggggttatggactggtgcc	120	
Db	97	ACTGGTGCTCTGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTCCC	156	
Qy	121	tcacctgaggacaggagagagatagtgctgtccccaaggaataatatccacc	180	
Db	157	TCACCTAGGGACAGGAGAGAGATAGTGTGTCTCCCAAGGAAAAATATATCCACC	216	
Qy	181	tcaaatataattcattgctgtaccagtgccacaagaagcaactactgtaccaatgactg	240	
Db	217	TCAAAATAATTTCGATTTCGTACCAAGTCCCAAGGAACCTACTGTCAATGACTG	276	
Qy	241	tccaggccgggaggatcacgactgcaggagtgtagagcggctcttcacgcgttc	300	
Db	277	TCCAGGCCGGGACGATACGGACTCCAGGGAAGTGAGAGCGGCTCTTCAOCGCTTC	336	
Qy	301	agaaacacactcagacactgcctcagctgtctccaaatgccaaaggaatgggtcaggt	360	
Db	337	AGAAACACCTCAGACACTGCCTCAGCTGCTCCAAATCCGAAAGAAATGGGTCAAGT	396	
Qy	361	ggagatctctttgcacgtgacccgggacacccgctgtgtgctgcagaaagaccagta	420	
Db	397	GGAGATCTCTTTCACAGTGGACCGGGACACCGTGTGGCTGCAGGAAGAACCCAGTA	456	
Qy	421	ccggcatattggagtgaacacctttccagtgcttcaattgcagcctctgctcaatgg	480	
Db	457	CCGCGCATATTGGAGTGAAACCTTTTCCAGTCTCTCAATTGCAGCCTCTGCCCTCAATGG	516	
Qy	481	gaccgtgcacctctctgccaggagaaacagacacccgtgtgcacctgcctgcaggttt	540	
Db	517	GACCGTGACCTCTCTTCCAGGAGAAACAGAACCCGTGTGCACCTGCCATGCAGGTTT	576	
Qy	541	ctttctaagaaacacgagtgtctctcctgtagttaactgaagaaagccttgagtgac	600	
Db	577	CTTTCTTAAGAGAAACAGAGTGTGTCTNCTGTAGTAACTGTAGAAAGGCTGGAGTGCA	636	
Qy	601	gaagttgtcctacccagattgagaatgttaagggcactgaggaactcaggcaccacagt	660	
Db	637	GAAGTTGTGCTACCCAGATTGAGAAATGTTAANGGCATGAGGACTCAGGACCACCAAT	696	
Qy	661	gctgtgtcccctggttcgt	679	
Db	697	GCTTGTGCGCCTGGNCAT	715	

RESULT	4				
LOCUS	AL577008				
DEFINITION	AL577008 LTI_NFL006_P12 Homo sapiens cDNA clone CS0D1082YA01 5 prime, mRNA sequence.	975 bp	mRNA	EST	16-FEB-2001
ACCESSION	AL577008				
VERSION	AL577008.1	GI:12939716			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1. (bases 1 to 975)				
TITLE	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.				
JOURNAL	Full-length cDNA libraries and normalization				
COMMENT	Unpublished (2001)				
	Contact: Genoscope				
	Genoscope - Centre National de Sequencage				

Db 891 TGCTGTTGCCCTGGTCATTTCTTTGGCTTTCC 925

RESULT 5

AL529836

LOCUS

DEFINITION

AL529836 LTI_NFL001_NBC4 Homo sapiens EST 13-FEB-2001

prime, mRNA sequence.

AL529836

ACCESSION

AL529836

VERSION

AL529836.1 GI:12793329.

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 942)

Li, W.B., Gruber, C., Jessee, J., and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

CONTACT: Genoscope

Genoscope - Centre National de Sequencage

Bp 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

Location/Qualifiers

1..942

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0DD005YP05"

/clone_lib="LTI_NFL001_NBC4"

/sex="male"

/tissue_type="neuroblastoma cells"

/lab_host="DH10B"

/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed

by Life Technologies. Contact : Feng Liang Life

Technologies, a division of Invitrogen 9800 Medical Center

Drive Rockville, Maryland 20850, USA Fax : (1) 301 610

8371 Email : fliang@lifetech.com, URL :

http://fulllength.invitrogen.com"

BASE COUNT 208 a 259 c 248 g 224 t 3 others

ORIGIN

Query Match 76.2%; Score 650.8; DB 106; Length 942;

Best Local Similarity 94.7%; Pred. No. 1.4e-164;

Matches 693; Conservative 2; Mismatches 35; Indels 2; Gaps 2;

QY 1 gactgagagccatagctgtctgcatggcctctccaccgtgctgacctgctgctgcc 60

|||||

Db 209 GAGTGAGAGCCATAGCTGTGTCATGGGCTCTCCACCGTGCCTGCTGCTGCC 268

|||||

QY 61 gctgggtgctcctgagctgtgtgggaatataccctcaggggtatttgactggtccc 120

|||||

Db 269 GCTGGTCTCTCGAGCTGTGTGGGAATATACCCCTCAGGGGTATTGACGTGCC 328

|||||

QY 121 tcacctgagggacaggagagagatgtgtgtctcccaaggaaatatatccacc 180

|||||

Db 329 TCACCTAGGGGACAGGAGAGAGATAGTGTGTCTCCCAAGGAAATATATCCACC 388

|||||

QY 181 tcaaaataattcattgtgtgtaccgaagtcccaaggaaacctactgtacatgactg 240

|||||

Db 389 TCAAAATAATTTCGATTTCGTACCAAGTCCCAAGGAACCTACTTGTACAAATGACTG 448

|||||

QY 241 tccagggccgggacgagatcacgactgagggagtgtgagcggtcccttcacggcttc 300

|||||

Db 449 TCCAGGCCCGGGGAGATACGACTCTCAGGGAGTGTGAGACGGGCTTCACCGGCTC 508

|||||

QY 301 agaaaaccacctcagacactgctcagctgtcccaatgccgaagaaatgggtcaggt 360

|||||

Db 509 AGAAACCACCTCAGACACTGCCTCAGCTCCTCAATGCCGAAGGAATGGTCAGGT 568

QY 361 ggagatctcttctgtcacagtggaccgggacacccgtgtgtggtgcaggaagaacagta 420

|||||

Db 569 GGAGATCTCTTCTTGTGCACAGTGGACCGGACACCGTGTGTGCTGCAGGAACAACAGTA 628

|||||

QY 421 ccggtattattggagtgaaaaaccttttccagtgttcattgagcctctgctcaatgg 480

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Db 629 CCGCATTTATTGGAGTGAAACCTTTTCCAGTCTTCAATTGCAGCCTCTGCCTCAATGG 688

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QY 481 gaccgtgcacctctcctgcagagaaacacacccgtgtgcacctgcctgcctgcaggg-tt 539

|||||

Db 689 GACCGTGACCTCTCTCCTCCAGGAGAAACACCGTGTGCACCTGCCATGCAAGTTT 748

|||||

QY 540 tcttttaagagaaaacagtggtgtctcctgttagtaactgttaagaaaagcctggagtgca 599

|||||

Db 749 TCTTCTTAAGAGAAACAGTGTGTCTCTCTGTAGTAAGTAAGGAGGAGGAGTGCA 808

|||||

QY 600 cgaagtgtgctacctaccacagattgagaattgtaaggagcactgagactcagcagcacag 659

|||||

Db 809 CG-AGTTGTGCTACCCAGATTGAGAAATGTAAGGGCACTGAGGACTCAGGCACACAG 867

|||||

QY 660 tgcgtgacctggtgtccctgcagcctttttcacagtgcatagcagttttttgt 719

|||||

Db 868 TCGTGTGCCCTCGTCATTTCTTTTGTGCTGTGCTTTTATMCTCTCTCTTCATGGTT 927

|||||

QY 720 tttgtttttgt 731

|||||

Db 928 TAATGTATCGCT 939

|||||

RESULT 6

BG180101

LOCUS

602329678F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4431019 5',

mrna sequence.

DEFINITION

BG180101

ACCESSION

BG180101.1 GI:12686804

VERSION

EST.

KEYWORDS

human.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 974)

NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE

Unpublished (1999)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10185 Row: g column: 20

High quality sequence stop: 657.

FEATURES

Location/Qualifiers

1..974

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4431019"

/clone_lib="NIH_MGC_91"

/tissue_type="adenocarcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: prostate; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally; oligo-dT primed.

Average insert size 1.4 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC Library."

BASE COUNT 259 a 265 c 265 g 185 t

ORIGIN

Query Match 75.4%; Score 643.6; DB 174; Length 974; Best Local Similarity 97.9%; Pred. No. 1.2e-162; Matches 652; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 29 ggcctctccacgcgtgctgaactgtctgctgcgcgtggtgctctctgagctgtgtggtggga 88
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Db 1 GGCCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTCTCTCTGGAGCTGTGGTGGGA 60
|||||
QY 89 atataccctcagggttattgagactggtccctcactcaggtgagacagagagagat 148
|||||
Db 61 ATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCCTAGGGGACAGGAGAGAGAT 120
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QY 149 agtgtgtgtcccaaggaaatatatccaccctcctcaaaataattcgattgtgtacccaag 208
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Db 121 AGTGTGTGTCCCAAGAAATATATCCACCCTCAAAATAATTGCGATTGCTGTACCAAG 180
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QY 209 tgcacaaaggaaactactgttacatgactgtccaggcccgccgggagagatacggactgc 268
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Db 181 TGCCACAAAGAACCTTACTTGTACATGACTGTCCAGGCCCGGGGAGGATACGGACTGC 240
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QY 269 agggagtgtgagcggctccctcaccgcttcagaaaaccactcagacactgcctcagc 328
|||||
Db 241 AGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAACACCTCAGACACTGCCTCAGC 300
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QY 329 tgcctcaaatgcgaaggaaatgggtcaggtggagatctctcttgccagtggtgaccgg 388
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Db 301 TGCTCCAAATGCCGAAGAAATGGTGCAGTGGAGATCTCTCTTGACAGTGGACCGG 360
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QY 389 gacacgctgtgtggtgcagggaaccagctaccggcattattggagtgaacaccttttc 448
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Db 361 GACACCGTGTGGTGTGAGGAGAACCACTACCGGCATTATTGGAGTGAACACCTTTTC 420
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QY 449 cagtgctcaattgagcctctgcctcaatgggacogtgcacacctctcctgcacaggagaa 508
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Db 421 CAGTGTCTCAATTTGACGCTCTGCCCTCAATGGGACCGTGCACCTCTCTCCGCCAGGAGAA 480
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QY 509 cagacacccgtgtgcctgcctgcatgaggtttcttcttaagagaaaacagtggtctcc 568
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Db 481 CAGAACACCGTGTGCACCTGCATGCAGGTTCCTTCTTAAGAGAAAACGAGTGTCTCC 540
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QY 569 ttagtaactgtaagaaagcgtgagtgacgacgaagtgtgctaccctcagattgagaat 628
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Db 541 TGTAGTAACTGTAAAGAAAGCTGGAGTGCACGAAGTTGTGCTACCCAGATTGAGAAAT 600
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QY 629 gtaagggcaactgaggaactcagggcaccacagtgctgtgtccctcgttccctcagacc 688
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Db 601 GTTAAAGGCACCTGAGGACTCAGGCACACAGTGTCTGTGCCCTGGTCAATTTCTTTGGTC 660
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RESULT 7

LOCUS AUI25021 845 bp mRNA EST 23-OCT-2000
DEFINITION AUI25021 NT2RM4 Homo sapiens cDNA clone NT2RM4000896 5', mRNA sequence.
ACCESSION AUI25021
VERSION AUI25021.1 GI:10949737
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 845)
AUTHORS Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and Isogai,T.
TITLE HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S., Isogai,T.)

JOURNAL COMMENT

Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES

source 1..845
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NT2RM4000896"
/clone_lib="NT2RM4"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/notes="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal precursor cells"
BASE COUNT 202 a 232 c 226 g 182 t 3 others
ORIGIN

Query Match 68.8%; Score 587.4; DB 107; Length 845;
Best Local Similarity 96.3%; Pred. No. 1.7e-147; Mismatches 19; Indels 5; Gaps 3;
Matches 632; Conservative 0

QY 1 gagtgcagagccatagctgtctgcatggcctctccacogtgcctgacctgctgctgcc 60
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Db 195 GAGTGAGAGCCCATAGCTGTGTCATGGGCTCTCCACCGTGCCTGACCTGTGCTGCC 254
|||||
QY 61 gctgtgtcctcctgagctgttggggaaataaccctcaggggttattgagctggtccc 120
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Db 255 ACTGGTCTCTGGAGCTGTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTCCC 314
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QY 121 tcacctagggaacagggagagagagatagtggtgtgtcccaagaaaataatccacc 180
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Db 315 TCACCTAGGGGGGAGGAGAGAGATAGTGTGTGTCCCAAGAAATATATCCACCC 374
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QY 181 tcaaaataattcattgtgtaccgaagtgcacaaaggaacctactgtgtaaatgactg 240
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Db 375 TCAAAATAATTCCATTGCTGTACCAAGTGCCACAAGGAACCTACTTGTACATGACTG 434
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QY 241 tcaggcccccgggcaggtacgcgactcagggagtgtagagcgcgtccttcacccgttc 300
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Db 435 TCCAGGCCCGGGCAGGATACGGACTGCAGGAGTGTGAGAGCGCTCTCTTACCGCTTC 494
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QY 301 agaaaaccacctcagacactgcctcagctcctcaaatgccgaagaaatgggtcaggt 360
|||||
Db 495 AGAAAACCACTCAGACACTGCCTCAGCTGTCTCCAAATGCCGAAGGAAATGGGTCAAGT 554
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QY 361 ggagatctcttctgacagtgacccgggacacogctgtgtgtgcaggaagaaacagta 420
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Db 555 GGAGATCTCTTCTGTCACAGTGGACCGGACACCGTGTGTGGCTGTCAGGAAAGACCACTA 614
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QY 421 ccggcattattgagtgaaaaacctttccagtgctcaattgcagcctctcctcaatgg 480
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Db 615 CCGGCATTATTGGAGTGAAAACCTTTTCCAGTGTCTCAATTGACAGCTCTCGCTCAATGG 674
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QY 481 gaccgtgcacctctcctgccaggagaaacagacacccgtgtgcacctgcctcaggtttt 540
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Db 675 GACCGTGACCTCTCTCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAAGTTT 734
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QY 541 ctttctaagagaaaacagtgctctcctctgttagtaactgtaagaaaagcctggagtgac 600
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Db 735 CTTTCTAAGAGAAAACGA-TGTGTCTNCTGTAGTAACTGTAAAGAAAAGCCTT-GAATGCA 792
|||||
QY 601 gaagtgtgcctaccctcagattgagaatgttaaggcagctgagacacagcaccac 656
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Db 793 GAAGTGTGCTCTACCC---ANATTGAAATGTTAAGGCACCTGAGGACTAGCACCACA 845
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RESULT 8
LOCUS AU142156 767 bp mRNA EST 25-OCT-2000
DEFINITION AU142156 THYR1 Homo sapiens cDNA clone THYR1001863 5', mRNA
sequence.
ACCESSION AU142156
VERSION AU142156.1 GI:11003677
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 767)
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamanoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
source Location/Qualifiers
1..767
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="THYR1001863"
/clone_lib="THYR1"
/tissue_type="thyroid gland"
/notes="Vector: pME18SFL3"
BASE COUNT 183 a 211 c 210 g 160 t 3 others
ORIGIN
Query Match 68.3%; Score 583.2; DB 108; Length 767;
Best Local Similarity 98.8%; Pred. No. 2.2e-146;
Matches 596; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
Qy 1 gagtgagagccatagctgtctggcattggggcctctccaccgtgctgacccgtgctgccc 60
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Db 166 GAGTGAGAGGCCATAGCTGTCTGGCATGGGCTCTCCACCGTGGCTGACCTGCTGCTGCC 225
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Qy 61 gctggtctcctgagctgttggtgggaataataccctcagggttattgactggtccc 120
|||||
Db 226 GCTGGTCTCTGTGAGCTGTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTCCC 285
|||||
Qy 121 tcacctaggagacaggagagagatagtggtgtccccaaggaataataccaccc 180
|||||
Db 286 TCACCTAGGGACAGGAGAGAGATAGTGTGTGTCCTCCCAAGGAAATATATCCACCC 345
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Qy 181 tcaaaataattcgatttctgtaccagtgcacaaaggacacctactgtacaatgactg 240
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Db 346 TCAAAATAATTCGATTGCTGTACCAAGTGCCACAAAGGAACCTACTGTACATGACTG 405
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Qy 241 tccaggccggggcagatagcagactgagggagtgtgagcgcgctctccaccgttc 300
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Db 406 TCCAGGCCGGGGCAGGATAGGACTGTCAGGAGTGTGAGAGCGGCTCC-TCACCGCTTC 464
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Qy 301 agaaaaccactagacactgcctcagctgtccaaatgccgaaggaatgggtcaagt 360
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Db 465 AGAAACACCACTCAGACACTGCCCTCAGCTGTCTCCAAATGCCGAAAGGAATGGGTCAGGT 524
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Qy 361 ggagatctcttcttgacagtggaccgggacacacgtgtgtggctgcaggaagaaccagta 420
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Db 314 ACTGCTCTCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGAGTGCTCC 373
Qy 121 tcaactagggagaggaagagatagtggtgtcccccaagaaataatatccaccc 180
Db 374 TCACCTAGGGACAGGAGAGAGATAGTGTGTCTCCCAAGGAATATATCCACCC 433
Qy 181 tcaaaataattgatttctgtctaccagtgcacaaagaaacctacttgtacaatgactg 240
Db 434 TCAAAATAATTGATTGTTGTGTACCAAGTGCACAAAGGAACCTACTTGTACAATGACTG 493
Qy 241 tccagcccgagagagatagctacagactcagagagtgtaagacggtctcctcacgcttc 300
Db 494 TCCAGCCCGGGGAGGATACCGACTGACGGAGGTGTGAGAGCGGCTCCTTCCACCGCTTC 553
Qy 301 agaaacacacctcagacactgctcagctgctccaaatgccaaagaaatgggtcaggt 360
Db 554 AGAAACACACCTCAGACACTGCTCAGCTGCTCCAAATGCCAGGAAGAAATGGTCAGGT 613
Qy 361 ggagatctcttcttgacagtgagccggagacccgtgtgtgtgctgcaggagaacagta 420
Db 614 GGAGATCTCTTCTTGCACAGTGGACGGGACACCCGTGTGTGGCTGCAGGAAGAACAGTA 673
Qy 421 ccggcatatggagtgaaacctttccagtgcttcaattgcagcctctgctcaatgg 480
Db 674 CCGGCATTATTGGAGTGAACCTTTTCCAGTGTCTCAATTGCAGCCTTGCTCAATGG 733
Qy 481 gaccgtgacacctctcgcaggagaacacagacacccgtgtgcacctgcatgcaggttt 540
Db 734 GACCGTGACCTT-TTCTGCCAGAGAAACAGAACACCGGTGCACCTGCCATGCAGGGTT 792
Qy 541 ctttctaaagaaaacagtggtgtctctgtagtactgtaactgaagaaaagcctgagtgac 600
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Qy 601 gaagttg 607
Db 853 CAAGTTG 859

RESULT 10
BE876920 971 bp mRNA EST 20-OCT-2000
LOCUS 601488490F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3890663 5',
DEFINITION mRNA sequence.
ACCESSION BE876920
VERSION BE876920.1 GI:10325683
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 971)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/PTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9674 row: d column: 24
High quality sequence stop: 722.
Location/Qualifiers
1. .971
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FEATURES
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Site.2: Sali; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
BASE COUNT 231 a 257 c 277 g 205 t 1 others
ORIGIN

Query Match 66.1%; Score 564.4; DB 141; Length 971;
Best Local Similarity 97.4%; Pred. No. 2.7e-141;
Matches 627; Conservative 0; Mismatches 11; Indels 6; Gaps 5;

Qy 1 gactgagagccatagctgtctggcatgggcccctccaccgtgctgacctgctgctgccc 60
Db 128 GAGTGAAGAGCCATAGCTGTCTGCATGGGCTCTCCACCGTGCCTGACCTGCTGCTGCC 187
Qy 61 gctggtgctcctgagctgtgtgggaataataaccctcaggggttattggactggctccc 120
Db 188 ACTGGTGTCTCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTCCC 247
Qy 121 tcaactagggagagagagagagatagtggtgtcccccaagaaataatatccaccc 180
Db 248 TCACCTAGGGGACAGGAGAGAGATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 307
Qy 181 tcaaaataattcatttctgtaccagtgcacaaagaaacctacttgtacaatgactg 240
Db 308 TCAAAATAATTGATTGCTGTACCAAGTGCACAAAGGAACCTACTTGTACAATGACTG 367
Qy 241 tccagcccgaggagagagactgcaggtgagaggtgtgagagcgtcctcctcacgcttc 300
Db 368 TCCAGGCCCGGGCAGGATACGGACTGCAGGAGTGTGAGAGCGGCTCCTTCCACCGCTTC 427
Qy 301 agaaacacacctcagacactgctcagctcctcaaatgccaaagaaatgggtcaggt 360
Db 428 AGAAACACCACTCAGACACTGCCTCAGCTGTCCAAATGCCAGGAAGAAATGGTGCAGGT 487
Qy 361 ggagatctcttctgcacagtgcacgggagacacgtgtgtgctgcaggagaacagta 420
Db 488 GGAGATCTCTTCTTGCACAGTGGACCGGACACCGTGTGTGTGTGTGTGTGTGTGTGT 547
Qy 421 ccggcattattgagtgaaaaccttttccagtgcttcaattgcagcctctgctcctcaatgg 480
Db 548 CCGGCATTATTGAGTGAACCTTTTCCAGTGTCTCAATTGCAGCCTCTG-CTCAATGG 606
Qy 481 gaccgtgacctctcctgcaggagaacacacacacacacacacacacacacacacacacac 540
Db 607 GACCGTGCACCTCTCCTGCCAGGAGAAACACACACCGTGTGTGTGTGTGTGTGTGTGTGT 666
Qy 541 ctttctaaag-aaaacgagtggtct-cctgtagtactgtaagaaaagcctgagtg 598
Db 667 CTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAAGAA--GCTGGAGTGC 724
Qy 599 acgaagtgtgctaccacacacacacacacacacacacacacacacacacacacacacac 642
Db 725 CGGAAGTTGTG-CTAACCCAGATTGAGATGTTTAGGCCCGAGA 767

RESULT 11
AUI37990
LOCUS AUI37990 772 bp mRNA EST 25-OCT-2000
DEFINITION AUI37990 PLACE1 Homo sapiens cDNA clone PLACE1007638 5', mRNA
sequence.
ACCESSION AUI37990
VERSION AUI37990.1 GI:10999511
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 772)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
AUTHORS
```



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Query Match      60.1%; Score 513.6; DB 108; Length 802;
Best Local Similarity 98.4%; Pred. No. 1.3e-127;
Matches 549; Conservative 0; Mismatches 6; Indels 3; Gaps 3;

QY 1 gagtgaagagccatagctgtctggcatggtggtcctctccaccgtgctgacctgctgctgcc 60
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DB 238 GAGTGAGAGGCCATAGCTGTGTCATGGGCTCTCCACCGTGCCTGACCTGCTGCTGCC 297
   |||

QY 61 gctggtctcctgagctgtgtggtggaataataccctcaggggtattgacaggtgcc 120
   |||
DB 298 ACTGCTCTCTGAGCTGTGTGGGAATATACCCCTCAGGGGTATTGAGCTGCTGCC 357
   |||

QY 121 tcacctgagggacaggagagagatagtggtgtcccaaggaaataataatccaccc 180
   |||
DB 358 TCACCTAGGGACAGGAGAGAGATAGTGTGTCTCCCAAGGAAATATATCCACCC 417
   |||

QY 181 tcaaaataattcgtattgctgacaaagtcacaaaggaaacctactgtacaatgactg 240
   |||
DB 418 TCAAAATAATTTCGATTTCGTACCAAGTGCACAAAGGAACCTACTTGTACAATGACTG 477
   |||

QY 241 tcacagccggggcagatcaggaactcagggagtgagagcgtctcctcaccgttc 300
   |||
DB 478 TCCAGGCCGGGGCAGGATACGGAGTGCAGGAGTGTGAGAGCGGCTCTTCACCGCTTC 537
   |||

QY 301 agaaacacacctcagacactgctcagctgctcctcctcctcctcctcctcctcctc 360
   |||
DB 538 AGAAACACCACTCAGACACTGCTCAGCTGCTCCAAATGCCGAAGGAAATGGTCAAGT 597
   |||

QY 361 ggagatctcttcttgcacagtgagacccggagacccgtgtgtgctgcagaagaaccagta 420
   |||
DB 598 GGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGCTGCGTGCAGGAAGAACAGTA 657
   |||

QY 421 ccggcattattgagtgaaaccttttccagtgcttcaattcagcctctgcctcaatgg 480
   |||
DB 658 CCGGCATATTGGAGTGAACACCTTTTTCAGTCTTCAATTGCAAGCTCTGGCTCAATGG 717
   |||

QY 481 gacctgacctctcctcctgaggaagaaacagaaacccgtgtgacctgacctgacctgttt 540
   |||
DB 718 GACCGTGCACTTCTCTGGC-AGGAGAACCGAACACCGTGTGCACTGGCATGCAGG-TT 774
   |||

QY 541 ctttctaagagaacacgagtggtg 563
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DB 775 CTTTCTAAGAGAAACGAGTGGG 797
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FEATURES
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/notes="vector: pME18SFL3; mRNA from uninduced NT2 neuronal precursor cells"
BASE COUNT 179 a 231 c 212 g 178 t 5 others
ORIGIN

Query Match      60.1%; Score 513.2; DB 107; Length 805;
Best Local Similarity 96.6%; Pred. No. 1.6e-127;
Matches 544; Conservative 0; Mismatches 16; Indels 3; Gaps 2;

QY 1 gagtgaagagccatagctgtctggcatggtggtcctctccaccgtgctgacctgctgctgcc 60
   |||
DB 238 GAGTGAGAGGCCATAGCTGTGTCATGGGCTCTCCACCGTGCCTGACCTGCTGCTGCC 297
   |||

QY 61 gctggtctcctgagctgtgtggtggaataataccctcaggggtattgacaggtgcc 120
   |||
DB 298 ACTGCTCTCTGAGCTGTGTGGGAATATACCCCTCAGGGGTATTGAGCTGCTGCC 357
   |||

QY 121 tcacctgagggacaggagagatagtggtgtcccaaggaaataataatccaccc 180
   |||
DB 358 TCACCTAGGGACAGGAGAGAGATAGTGTGTCTCCCAAGGAAATATATCCACCC 417
   |||

QY 181 tcaaaataattcgtattgctgacaaagtcacaaaggaaacctactgtacaatgactg 240
   |||
DB 418 TCAAAATAATTTCGATTTCGTACCAAGTGCACAAAGGAACCTACTTGTACAATGACTG 477
   |||

QY 241 tcacagccggggcagatcaggaactcagggagtgagagcgtctcctcaccgttc 300
   |||
DB 478 TCCAGGCCGGGGCAGGATACGGAGTGCAGGAGTGTGAGAGCGGCTCTTCACCGCTTC 537
   |||

QY 301 agaaacacacctcagacactgctcagctgctcctcctcctcctcctcctcctcctc 360
   |||
DB 538 AGAAACACCACTCAGACACTGCTCAGCTGCTCCAAATGCCGAAGGAAATGGTCAAGT 597
   |||

QY 361 ggagatctcttcttgcacagtgagacccggagacccgtgtgtgctgcagaagaaccagta 420
   |||
DB 598 GGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGCTGCGTGCAGGAAGAACAGTA 657
   |||

QY 421 ccggcattattgagtgaaaccttttccagtgcttcaattgacagcctcctcctcaatgg 480
   |||
DB 658 CCGCATATTTCGAGTGAACACCTTTT-CAGTGTCTTCAATTGCAAGCTCTGGCTCAATGG 716
   |||

QY 481 gacctgacctctcctcctgaggaagaaacacacccgtgtgacctcctcctcaggttt 540
   |||
DB 717 GACCGNCACTTNT-CTGGCAGGAGAAACAGAACACCGTGTGCACTGGCATGCAGG-TT 774
   |||

QY 541 ctttctaagagaacacga 558
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DB 775 CTTTCTAAGAGAAACGA 792
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RESULT 15
AUI25694
LOCUS      805 bp mRNA EST 23-OCT-2000
DEFINITION AUI25694 NT2RM4 Homo sapiens cDNA clone NT2RM4002028 5', mRNA
sequence.
ACCESSION AUI25694
VERSION AUI25694.1 GI:10950410
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 805)
AUTHORS Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J.,
Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
Isogai,T.
TITLE HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S.,
Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki
,Y., Sugano,S., Isogai,T.)
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
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Search completed: August 14, 2001, 05:58:16
Job time: 1293 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2001, 05:35:08 ; Search time 20.59 Seconds
(without alignments)
1407.227 Million cell updates/sec

Title: US-09-599-400A-9

Perfect score: 1231

Sequence: 1 MGLSTVPDLLPLVLELLV.....ENVKGTEDSGTTLPLVRP 219

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL16:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	873	70.9	189	6	Q97530 canis famil
2	866	70.3	189	6	Q95185 felis silve
3	213	17.3	380	4	Q00280 homo sapien
4	208	16.9	253	4	Q00276
5	208	16.9	418	4	Q00275
6	205.5	16.7	277	4	O14866
7	205.5	16.7	426	4	O14865
8	204	16.6	417	11	Q920W1
9	203.5	16.5	175	4	Q9UME5
10	203.5	16.5	178	4	Q9UME0
11	203.5	16.5	181	4	Q9UME1
12	200.5	16.3	147	11	Q9ER63
13	199.5	16.2	357	13	Q9DF34
14	199	16.2	387	13	Q9PVD4
15	198.5	16.1	141	11	Q9ER62
16	188	15.3	302	13	Q9PUS0
17	182.5	14.8	285	13	Q9DGH7
18	179	14.5	320	14	O57079
19	179	14.5	322	14	O72761

20	176	14.3	459	11	Q62327	mus musculus
21	175.5	14.3	312	13	Q9DGH8	gallus gallus
22	174.5	14.2	320	14	O57091	ectromelia
23	174.5	14.2	320	14	O57300	ectromelia
24	174.5	14.2	347	14	O57119	cowpox viru
25	174	14.1	347	14	O57115	cowpox viru
26	174	14.1	350	14	O57123	cowpox viru
27	174	14.1	351	14	O57121	cowpox viru
28	173.5	14.1	438	13	Q9DFV0	brachydanio
29	172.5	14.0	349	14	O57100	monkeypox v
30	172.5	14.0	360	14	O57118	cowpox viru
31	171.5	13.9	316	14	O57092	ectromelia
32	171.5	13.9	348	14	O57277	monkeypox v
33	171.5	13.9	482	11	O88734	mus musculus
34	171	13.9	349	14	O57305	cowpox viru
35	171	13.9	355	14	O85308	cowpox viru
36	169.5	13.8	348	14	O57103	monkeypox v
37	169.5	13.8	348	14	O57108	monkeypox v
38	169	13.7	326	14	O57120	cowpox viru
39	169	13.7	351	14	O73559	cowpox viru
40	168	13.6	372	4	Q9UHP4	homo sapien
41	168	13.6	401	4	O00300	homo sapien
42	167.5	13.6	349	14	O57291	monkeypox v
43	167.5	13.6	349	14	O57099	monkeypox v
44	167.5	13.6	349	14	O57101	monkeypox v
45	167.5	13.6	349	14	O57102	monkeypox v

ALIGNMENTS

RESULT 1

O97530 ID O97530 PRELIMINARY; PRT: 189 AA.
AC O97530;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Duthie S., Nasir L., Argyle D.J., Eckersall P.D.;
RT "Canine tumor necrosis factor receptor, partial cds.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF013955; AAD01516.1; -
DR HSSP; P19438; TNFR.
DR InterPro; IPR000561; -
DR InterPro; IPR001368; -
DR Pfam; PF00020; TNFR_c6; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR SMART; SM00208; TNFR; 1.
KW Receptor.
FT NON_TER 189 189
SQ SEQUENCE 189 AA; 21324 MW; 5D3AD6A5676BFE99 CRC64;

Query Match 70.9%; Score 873; DB 6; Length 189;

Best Local Similarity 81.9%; Pred. No. 2.5e-83;

Matches 154; Conservative 11; Mismatches 23; Indels 0; Gaps 0;

Qy 1 MGLSTVPDLLPLVLELLVGVSGVGLVPHLGDREKRDSCVQGYIHQNNISICT 60

Db 1 MGLPTVPGLLPLVLLLELLVPSVTALVPHPRNRKRAILCPQGYIHPDDISICT 60

Qy 61 KCHGTYLNDPCPGQDTCDECEGSGFTASENHLRHCLSCSKCKEMGQVEISSCTVD 120

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Db 61 KHKGTLYLNDGPGGLDTCRECEGTFTASENHLRQCLSCSKCRKEMNOVEISPCTVY 120
Qy 121 RDTVCGCRKNQYRHVWSENLFCFNCISLCLNGTVHLSCOEKQNTVCTCHAGFFLRNECV 180
Db 121 RDTVCGCRKNQYRHVWSENLFCFNCISLCLNGTVHLSCOEKQNTVCTCHAGFFLRNECV 180
Qy 181 SCSNCKKS 188
Db 181 SCVNCKKN 188

RESULT 2
Q95185 ID Q95185 PRELIMINARY; PRT; 189 AA.
AC Q95185;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE TUMOUR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).
GN TNFR-1.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID-9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Duthie S., Nasir L., Eckersall P.D.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U72344; AAB95089.1; -.
DR HSSP; P19438; 1EXT.
DR InterPro; IPR000561; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00200; TNFR_C6; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
DR SMART; SM00208; TNFR; 1.
FT NON_TER 189
SQ SEQUENCE 189 AA; 21420 MW; F3FBE0CE809D7DBE CRC64;

Query Match 70.3%; Score 866; DB 6; Length 189;
Best Local Similarity 82.4%; Pred. No. 1.3e-82;
Matches 155; Conservative 8; Mismatches 25; Indels 0; Gaps 0;

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Db 1 MGLPTVPGLLQPLVLLALLVEIYPLVGLVPHLRDRRAIYPCPGKYIHPQDNISICT 60

Qy 61 KHKGTLYLNDGPGGLDTCRECEGTFTASENHLRQCLSCSKCRKEMNOVEISPCTVD 120
Db 61 KHKGTLYLNDGPGGLDTCRECEGTFTASENHLRQCLSCSKCRKEMNOVEISPCTVY 120

Qy 121 RDTVCGCRKNQYRHVWSENLFCFNCISLCLNGTVHLSCOEKQNTVCTCHAGFFLRNECV 180
Db 121 RDTVCGCRKNQYRHVWSENLFCFNCISLCLNGTVHLSCOEKQNTVCTCHAGFFLRNECV 180

Qy 181 SCSNCKKS 188
Db 181 SCVNCKKN 188

RESULT 3
ID Q00280 PRELIMINARY; PRT; 380 AA.
AC Q00280;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE LYMPHOCTE ASSOCIATED RECEPTOR OF DEATH 9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Db 61 KHKGTLYLNDGPGGLDTCRECEGTFTASENHLRQCLSCSKCRKEMNOVEISPCTVY 120
Qy 121 RDTVCGCRKNQYRHVWSENLFCFNCISLCLNGTVHLSCOEKQNTVCTCHAGFFLRNECV 180
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Qy 181 SCSNCKKS 188
Db 181 SCVNCKKN 188

RESULT 4
ID Q00276 PRELIMINARY; PRT; 253 AA.
AC Q00276;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE LYMPHOCTE ASSOCIATED RECEPTOR OF DEATH 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Medline-9727273; PubMed-9114039;
RA Sreaton G.R., Xu X.N., Olsen A.L., Cowper A.E., Tan R.,
RA McMichael A.J., Bell J.I.;
RT "LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
DR EMBL; U94503; AAC51308.1; -.
DR HSSP; P19438; 1EXT.
DR InterPro; IPR000561; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00200; TNFR_C6; 2.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.

Query Match 17.3%; Score 213; DB 4; Length 380;
Best Local Similarity 28.3%; Pred. No. 3e-14;
Matches 65; Conservative 24; Mismatches 95; Indels 46; Gaps 11;

Qy 15 LLELLGIYPSGVIGLVPHLGDREKRDVCPQGYIHPQNNISICTKCHKGTLYLNDGPG 74
Db 15 LLLVLIGARAQG-----GTRSPR---CDCAGDFHKKIGLFCRCGCPAGHYLKAPCTE 63

Qy 75 PGQDTDCRECEGTFTASENHLR-HCLSCSKCRKEMQVEISSCTVDRTVCGCRKNQYR 133
Db 75 PGQDTDCRECEGTFTASENHLR-HCLSCSKCRKEMQVEISSCTVDRTVCGCRKNQYR 133

Qy 64 PCGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVALENCASAVADFCGCKPGWF 123
Db 64 PCGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVALENCASAVADFCGCKPGWF 123

Qy 134 HYWSENLFQC-----FNCISLCLN-GTVH-----LSCQEKQNTVCTCHAGFFLRNECVSC- 182
Db 124 EC---QVSSQCVSSSPFYCQPCLDGALHRLHTRLCISRRDTCGCTCLPGFYEHGDCVSCP 180

Qy 183 ----SNCKSLECKLCLPOIENVKGT-----DSGTTVLLP 215
Db 181 TSTLGSCE--RCAAVC-GWRQNEAGMEALTPPPATHLSPDLSAHTLLAP 227

RESULT 5
ID Q00276 PRELIMINARY; PRT; 253 AA.
AC Q00276;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE LYMPHOCTE ASSOCIATED RECEPTOR OF DEATH 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Medline-9727273; PubMed-9114039;
RA Sreaton G.R., Xu X.N., Olsen A.L., Cowper A.E., Tan R.,
RA McMichael A.J., Bell J.I.;
RT "LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
DR EMBL; U94503; AAC51308.1; -.
DR HSSP; P19438; 1EXT.
DR InterPro; IPR000561; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00200; TNFR_C6; 2.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
```

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DR SWART: SM00208; TNFR; 1.
SQ SEQUENCE 253 AA; 26934 MW; 4CD06775B68E9292 CRC64; 9;

Query Match 16.9%; Score 208; DB 4; Length 253;
Best Local Similarity 28.9%; Pred. No. 6.7e-14;
Matches 57; Conservative 22; Mismatches 86; Indels 32; Gaps

QY 15 LLELLVGYPGVLGVLPHLGDREKRDVCPQGYIHPQNNISICCTKCHKGTLYLNDPCG 74
   ||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 15 LLLVLLGARAQG-----GTRSPR---CDCAGDFHKKIGLFCRCGCPAGHYLKAPCTE 63

QY 75 PGQDTRCECSGFTASENHLR-HCLSCSKCREMGQVEISSCTVDTRDTCVGCCKNOYR 133
   | : : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 64 PCGNSTCLVCPQDFTLAWENHNNSECARCQACDQASQVALENGSAVADTRCGCKPGWVF 123

QY 134 HYWSENLFQC-----FNCISCLN-GTVH-----LSCQEKONTVCTCHAGFFLRENCVSC- 182
   || : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 124 EC---QVSSQCVSSPFFVCPCLDCGALHRTRLCSRRDTCGTLCPGYEHGDCVSCP 180

QY 183 ----SNCKKSLECTKLC 195
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 181 TSTLGSCPEN--RCAAVC 195

RESULT 5
O00275 PRELIMINARY; PRT; 418 AA.
AC O00275;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9727273; PubMed=9114039;
RA Sreaton G.R., Xu X.N., Olsen A.L., Cowper A.E., Tan R.,
RA McMichael A.J., Bell J.I.;
RT "LARD: a new lymphoid-specific death domain containing receptor
RT regulated by alternative pre-mRNA splicing.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
DR EMBL; U94502; AAC51307.1; -
DR HSSP; P19438; 1EXT.
DR InterPro; IPR000488; -
DR InterPro; IPR000561; -
DR InterPro; IPR001368; -
DR Pfam; PF00020; TNFR_c6; 2.
DR Pfam; PF00531; death; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
DR SMART; SM00005; DEATH; 1.
SQ SEQUENCE 418 AA; 45456 MW; 54B48F8B35C620E2 CRC64;

Query Match 16.9%; Score 208; DB 4; Length 418;
Best Local Similarity 28.9%; Pred. No. 1.1e-13;
Matches 57; Conservative 22; Mismatches 86; Indels 32; Gaps

QY 15 LLELLVGYPGVLGVLPHLGDREKRDVCPQGYIHPQNNISICCTKCHKGTLYLNDPCG 74
   ||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 15 LLLVLLGARAQG-----GTRSPR---CDCAGDFHKKIGLFCRCGCPAGHYLKAPCTE 63

QY 75 PGQDTRCECSGFTASENHLR-HCLSCSKCREMGQVEISSCTVDTRDTCVGCCKNOYR 133
   | : : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 64 PCGNSTCLVCPQDFTLAWENHNNSECARCQACDQASQVALENGSAVADTRCGCKPGWVF 123

QY 134 HYWSENLFQC-----FNCISCLN-GTVH-----LSCQEKONTVCTCHAGFFLRENCVSC- 182
   || : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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[illegible]


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Db 123 NTVCs 127

RESULT 13
Q9DF34
ID Q9DF34 PRELIMINARY; PRT; 357 AA.
AC Q9DF34
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
DE DEATH RECEPTOR.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Long Q., Huang H., Shafizadeh E., Liu N., Lin S.;
RT "Stimulation of erythropoiesis by inhibiting a new hematopoietic death
  receptor in transgenic zebrafish."
RL Nat. Cell Biol. 0:0-0(2000).
DR EMBL; AF302789; AAG21396.1; -.
KW Receptor.
SQ SEQUENCE 357 AA; 40662 MW; 1652B48409EEDBA CRC64;

Query Match 16.2%; Score 199.5; DB 13; Length 357;
Best Local Similarity 27.6%; Pred. No. 7.2e-13;
Matches 60; Conservative 27; Mismatches 79; Indels 51; Gaps 9;

QY 10 LPLVLELLVGYPSGVLGVPH-LGDREKRDSPQGV-KYIHPQNNISCTCKCHKGT 67
  ||| ||| : : : : : ||| : : : : : |||
Db 6 LVLVLLLVNINARSHGLAWAHSVKNRLSDVSCREGLYEPH---ENICCLNCPAGTY 62

QY 68 LYNDCPGQDPTDCRCESGFTASENHLRHLCSKCKEMQGVESCTVDRDVTVC 127
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 VRKACAAAAGKVCAPCEFTYTHDHLGLKICSDCKR--IDQETIEKCTSTQNTCKC 120

QY 128 RKNQYRHYWSENLFQCFNCSLCLNGTVHLSQCEKQNTVCTCHAGFLRENEVCVSCNCK 187
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 R-----NGSFCL-----PQAC-----EVCCKKSRCKE 143

QY 188 SLECKLCL-----LPQIENVKGTEDSGT-TVLLPLV 217
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 144 DEETKSCRTAISTVCKRNSPGSSFTSWFIVIMPLI 180

RESULT 14
Q9PVD4
ID Q9PVD4 PRELIMINARY; PRT; 387 AA.
AC Q9PVD4
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
DE P75-LIKE TRANSMEMBRANE PROTEIN FULLBACK.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Hick E., Sun B.I., Collins-Racie L., Lavallie E., Sive H.L.;
RT "Identification and Characterization of fullback, a Novel Posteriorly-
  Expressed Xenopus Gene."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF131890; AAD54072.1; -.
DR HSSP; P07174; 1NGR.
DR InterPro; IPR000488; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_c6; 4.
DR Pfam; PF00531; death; 1.

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DR PROSITE; PS50017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_3.
DR PROSITE; PS00050; TNFR_NGFR_2; 4.
DR SMART; SMO0005; DEATH; 1.
KW Transmembrane.
SQ SEQUENCE 387 AA; 42066 MW; 1A386A239C7C8A82 CRC64;

Query Match 16.2%; Score 199; DB 13; Length 387;
Best Local Similarity 29.1%; Pred. No. 8.7e-13;
Matches 65; Conservative 32; Mismatches 84; Indels 42; Gaps 13;

QY 12 PLYLLELLVGYPSGVLGVPHLGDREKRDSPQGVKYPQNNISCTCKCHKGTLYND 71
  ||| ||| : : : : : ||| : : : : : |||
Db 6 PIVTLCILL-----LISKISAEDVCSGLY---TNSGKCCSLCPAGFGVVVP 49
  ||| ||| : : : : : ||| : : : : : |||

QY 72 CPGPQDPTDCREC-ESGFTASENHLRHLCSKCKEMQGVESCTVDRDVTVCGRKN 130
  ||| ||| : : : : : ||| : : : : : |||
Db 50 C-GDSDTKCEPCIENSTFSDVRSKAKACQPCFTQSPSLTLE-SNCTREQDVTVCRCPE 106
  ||| ||| : : : : : ||| : : : : : |||

QY 131 QYRHYWSENLFQCFNCSLCLNG-TVHLSQCEKQNTVCTCHAGFLR-----ENECVSC-S 183
  ||| ||| : : : : : ||| : : : : : |||
Db 107 QYLD--SNGI--CLPQCLCKSGHGVSCQTHNKNTVCLCSGSGFYSEVKSSEPCLPCT 162
  ||| ||| : : : : : ||| : : : : : |||

QY 184 NCKKSLCTKLCPLQ-----IENVKGTPE--DSGTTVLLP 215
  ||| ||| : : : : : ||| : : : : : |||
Db 163 ECKETEVOIGDVPQHDILCMKDKVPILKRTGEGGNGTSAGSP 205

RESULT 15
Q9ER62
ID Q9ER62 PRELIMINARY; PRT; 141 AA.
AC Q9ER62;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR P60 HOMOLOGUE 2.
GN TNFRH2.
OS Mus musculus domesticus (western European house mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10092;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20519229; PubMed=11063728;
RA Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,
  Lane N., Reik W., Walter J.;
RT "Sequence and functional comparison in the Beckwith-Wiedemann region:
  Implications for a novel imprinting centre and extended imprinting."
RL Hum. Mol. Genet. 9:2691-2706(2000).
DR EMBL; AJ278265; CAC16406.1; -.
KW Receptor.
SQ SEQUENCE 141 AA; 15576 MW; 7552DE3E8EA8E5F3 CRC64;

Query Match 16.1%; Score 198.5; DB 11; Length 141;
Best Local Similarity 32.8%; Pred. No. 3.7e-13;
Matches 41; Conservative 18; Mismatches 59; Indels 7; Gaps 4;

QY 44 CPOGKYIHPQNNISCTCKCHKGTLYNDPQGPQDPTDCRECESGFTASENHLRHLCS 103
  ||| ||| : : : : : ||| : : : : : |||
Db 9 CPAGEY---WSKDYCKKNCNSAGTFVAPCEIPHTQGCCKCHPGTTFTEKDYLDACILCS 65
  ||| ||| : : : : : ||| : : : : : |||

QY 104 KCRKEMQGVESCTVDRDVTVCGRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSQCEKQ 162
  ||| ||| : : : : : ||| : : : : : |||
Db 66 TCDDK--QEMVADCSATSDRCKQCRTGLY-YDYPKFPESCRPCTKCPQGIPLVQECNSTA 122
  ||| ||| : : : : : ||| : : : : : |||

QY 163 NTVCT 167
  ||| ||| : : : : : ||| : : : : : |||
Db 123 NTVCs 127

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Search completed: August 14, 2001, 05:38:06
Job time: 178 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2001, 05:28:03 ; Search time 18.64 Seconds

(without alignments)

712.267 Million cell updates/sec

Title: US-09-599-400A-9

Perfect score: 1231

Sequence: 1 MGLSTVPDLLPLVLELLV.....ENVKGTEDSGTTLPLVLRP 219

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_0601.*

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- 2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT.*
- 3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT.*
- 4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT.*
- 5: /SIDSL/gcgdata/geneseq/geneseq/AA1984.DAT.*
- 6: /SIDSL/gcgdata/geneseq/geneseq/AA1985.DAT.*
- 7: /SIDSL/gcgdata/geneseq/geneseq/AA1986.DAT.*
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- 20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT.*
- 21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT.*
- 22: /SIDSL/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1219	99.0	280	22	Tnfr1 protein. Un
2	1219	99.0	371	11	Tumour Necrosis fa
3	1219	99.0	455	12	30kD TNF inhibitor
4	1219	99.0	455	12	Human 55kD TNF-bin
5	1219	99.0	455	13	TNF-alpha 55kD rec
6	1219	99.0	455	14	Lambda derived TNF
7	1219	99.0	455	16	p55 TNF-R. Homo s
8	1219	99.0	455	20	Human tumour necro
9	1219	99.0	455	21	Human tumour necro
10	1219	99.0	455	21	Human TNFR 1. Hom
11	1219	99.0	455	21	Human TNFR 1. Hom

12	1219	99.0	455	21	AA233446
13	1219	99.0	455	21	AA233446
14	1219	99.0	455	22	AA233446
15	1219	99.0	455	22	AA233446
16	1213	98.5	455	13	AA20787
17	1210	98.3	433	14	AA251032
18	1210	98.3	443	14	AA251033
19	1210	98.3	455	14	AA242197
20	1210	98.3	455	14	AA251034
21	1209	98.2	455	12	AA212550
22	1208.5	98.2	909	19	AA264485
23	1203	97.7	455	11	AA207451
24	1192	96.8	211	20	AA289225
25	1192	96.8	311	20	AA289229
26	1192	96.8	366	20	AA289228
27	1192	96.8	397	20	AA289227
28	1192	96.8	417	20	AA289226
29	1192	96.8	420	20	AA289224
30	1189	96.6	453	22	AA250895
31	1130	91.8	199	13	AA24080
32	1089	88.5	309	16	AA270108
33	1089	88.5	451	16	AA270107
34	1089	88.5	547	16	AA270104
35	1089	88.5	900	16	AA270103
36	1088	88.4	1245	16	AA270106
37	1088	88.4	1604	16	AA270105
38	999	81.2	884	16	AA270109
39	992.5	80.6	336	18	AA233360
40	979	79.5	285	18	AA233359
41	946	76.8	168	13	AA24084
42	941	76.4	161	13	AA27496
43	941	76.4	161	19	AA259664
44	941	76.4	161	19	AA252267
45	941	76.4	161	20	AA289233

ALIGNMENTS

RESULT 1

AA2866979
ID AA2866979 standard; Protein; 280 AA.

XX AA2866979;

XX 19-APR-2001 (first entry)

DT Tnfr1 protein.

DE XX

XX Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;

XX multiple sclerosis; osteoporosis; asthema; inflammation;

XX systemic lupus erythematosus; graft-versus-host disease; septic shock;

XX acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;

XX coronary condition; myocardial infarction; cancer; diabetes; psoriasis;

XX endometriosis; fever; glomerulonephritis; inflammatory bowel disease;

XX ischaemia; Parkinson's disease.

XX Unidentified.

XX OS

XX WO200103719-A2.

XX 18-JAN-2001.

XX 07-JUL-2000; 2000WO-US18667.

XX 09-JUL-1999; 99US-0350670.

XX 09-DEC-1999; 99US-0457647.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;

XX WPI; 2001-103031/11.

XX

XX

XX

XX Treating conditions leading to bone loss such as rheumatoid arthritis,
 PT multiple sclerosis and asthma, comprises administering an
 PT osteoprotegerin protein in conjunction with e.g. inhibitors of
 PT interleukin and tumor necrosis factor alpha
 XX Disclosure; Fig 2; 316pp; English.

XX The present invention relates to a method for treating conditions leading
 CC to bone loss. The method comprises administering a purified and isolated
 CC osteoprotegerin (OPG) protein (AA057836-AA057838 and AA066974-AA066976)
 CC in conjunction with other substances such as tumour necrosis factor-alpha
 CC (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE
 CC modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet
 CC activating factor (PAF) antagonists. The method is useful for treating
 CC conditions leading to bone loss such as rheumatoid arthritis, multiple
 CC sclerosis, osteoporosis, osteomyelitis and asthma. The method is also
 CC useful for treating inflammation, systemic lupus erythematosus (SLE) and
 CC graft-versus-host disease (GVHD). Other diseases that can be treated
 CC include acute pancreatitis, Alzheimer's disease, anorexia,
 CC atherosclerosis, coronary conditions (e.g. myocardial infarction),
 CC cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,
 CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,
 CC psoriasis and septic shock. The present sequence was used in a sequence
 CC homology comparison.

XX Sequence 280 AA;

Query Match 99.0%; Score 1219; DB 22; Length 280;
 Best Local Similarity 100.0%; Pred. No. 1.2e-91;
 Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLLPLVLELLVGIYPSGVIGLVPHLGRDSDVCPQKVIHPQNNISICT 60
 DB 1 mglstvpdlllplvlellvgiypsgviglvphlgdrdsdvcpgkylhpnnsicct 60
 QY 61 KCHKGTLYNDPCPGQDTCRECEGSGFTASENHLRHCLSCSKCRKEMGOVEISSCTVD 120
 DB 61 kchkgtlyndpcpgqgdtcrecesgftasenhhlrhclscskcrkemgoveissctvd 120
 QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180
 DB 121 rdtvcgrknqyrhywsenlfqcfncslclngtvhlscqekqntvctchagfflrenecv 180
 QY 181 SCSCNCKKSLCTKLCPLQIENVKGTEDSGTTLPLV 217
 DB 181 scsnckkslectklcplqienvkgtdsgttvllplv 217

RESULT 2
 AAR07449
 ID AAR07449 standard; protein; 371 AA.
 AC AAR07449;
 XX
 XX
 XX
 XX 29-JAN-1991 (first entry)
 DE Tumour Necrosis Factor-Binding Protein from pTNF-BP15 cDNA.
 DE Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
 KW pTNF-BP15; infectious disease; parasitic disease; cachexia;
 KW autoimmune disease; shock.

XX Homo sapiens.
 OS
 XX EP393438-A.
 PN
 XX 24-OCT-1990.
 PD
 XX 06-APR-1990; 90EP-0106624.
 PF
 XX 21-JUN-1989; 89DE-3920282.
 PR

PR 21-APR-1989; 89DE-3913101.
 XX
 XX (BOEH) BOEHRINGER INGELHEIMINT.
 PA
 XX Hauptmann R, Himmeler A, Maurer-Fogy I, Stratowa C;
 PI
 XX WPI; 1990-321987/43.
 DR N-PSDB; AAQ06282.

XX DNA encoding TNF binding protein and TNF- receptor - used in
 PT tumour treatment and to understand mechanisms to TNF action
 XX Disclosure; Fig 1(1-3); 51pp; German.
 XX Clone pTNF-Bp15 was used to construct pADTNF-BP, for transfection of
 CC e.g. COS7 cells. The expressed proteins are useful
 CC prophylactically and therapeutically to control disorders which
 CC involve the damaging effects of TNF-alpha or -beta (e.g. infectious or
 CC parasitic diseases, shock, cachexia, autoimmune diseases, adult
 CC respiratory distress syndrome etc., or side effects of treatment with
 CC TNF-alpha). They can also be used as diagnostic reagents for
 CC assaying TNF and in study of TNF-receptor interactions.
 CC See also AAQ06282-Q06285.

XX Sequence 371 AA;

Query Match 99.0%; Score 1219; DB 11; Length 371;
 Best Local Similarity 100.0%; Pred. No. 1.6e-91;
 Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLLPLVLELLVGIYPSGVIGLVPHLGRDSDVCPQKVIHPQNNISICT 60
 DB 1 mglstvpdlllplvlellvgiypsgviglvphlgdrdsdvcpgkylhpnnsicct 60
 QY 61 KCHKGTLYNDPCPGQDTCRECEGSGFTASENHLRHCLSCSKCRKEMGOVEISSCTVD 120
 DB 61 kchkgtlyndpcpgqgdtcrecesgftasenhhlrhclscskcrkemgoveissctvd 120
 QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180
 DB 121 rdtvcgrknqyrhywsenlfqcfncslclngtvhlscqekqntvctchagfflrenecv 180
 QY 181 SCSCNCKKSLCTKLCPLQIENVKGTEDSGTTLPLV 217
 DB 181 scsnckkslectklcplqienvkgtdsgttvllplv 217

RESULT 3
 AAR10986
 ID AAR10986 standard; Protein; 455 AA.
 XX
 AC AAR10986;
 XX
 XX 13-MAY-1991 (first entry)
 DT
 XX 30kD TNF inhibitor precursor.
 DE
 XX Tumour necrosis factor; inhibitor.
 KW
 XX Homo sapiens.
 OS
 XX Key
 FT Cleavage-site 40..41
 FT note=" cleavage gives active protein "
 FT
 XX AU9058976-A.
 PN
 XX 24-JAN-1991.
 PD
 XX 16-JUL-1990; 90AU-0058976.
 PF
 XX 07-FEB-1990; 90US-0479661.
 PR

PR 18-JUL-1989; 89US-0381080.
 PR 11-DEC-1989; 89US-0450329.

PA (SYNE-) SYNERGEN INC.

XX WPI; 1991-073847/11.

DR N-PSDB; AAQ10883.

XX Tumour necrosis factor inhibitor - for suppression of TNF-alpha
 and -beta, useful as therapeutic agent.

PS Disclosure; Fig 21; 142pp; English.

XX The sequence comprises the entire 30 kD TNF inhibitor. The clone
 CC from which the sequence was deduced was isolated from a cDNA
 CC library prepd. from RNA form U937 cells treated with PMA/PHA.
 CC The whole gene can be inserted into expression vectors for prepn.
 CC of TNF inhibitor for use in the treatment of inflammatory and
 CC degenerative diseases. The active protein is claimed (Claim 8).
 CC See also AAR10984 and AAR11001.

XX Sequence 455 AA;

Query Match 99.0%; Score 1219; DB 12; Length 455;
 Best Local Similarity 100.0%; Pred. No. 2e-91;

Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLPHLGDRKDSVCPQGYIHPQNSICT 60
 DB 1 mglstvpdllplvlellvgyipsgviglphlgdrkrdsvcpqgyihpqnnsict 60

QY 61 KCHKGTLYLNDPCPGQDTCRECSGSFTASENHLRHLCSKCRKEMQVEISSCTVD 120
 DB 61 kchkgtlylndpcpgqgtdcrecsgsftasenhrlhrlcsckrkemqgveissctvd 120

QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQEKONTVCTCHAGFFLRNECV 180
 DB 121 rdtvcgcrknqyrhywsenlfqcfncslcngtvlhlsceqkntvctchagfflrenecv 180

QY 181 SCSCNCKKSLCTKCLPQIENVKGTEDSGTTVLLPLV 217
 DB 181 scsnckkslectkclpqienvkgtedsdgttvlplv 217

RESULT 4

AAR11082
 ID AAR11082 standard; Protein; 455 AA.

XX AC AAR11082;

DT 24-MAY-1991 (first entry)

XX Human 55kD TNF-binding protein.

XX Tumour Necrosis Factor; binding proteins; septic shock;
 KW autoimmune glomerulonephritis; lymphokine; cytokine.

XX Key Location/Qualifiers

FT Modified-site 54 /label= putative N-glycosylation site

FT Modified-site 145 /label= putative N-glycosylation site

FT Modified-site 151 /label= putative N-glycosylation site

FT Modified-site 270 /label= putative N-glycosylation site

FT Region 212..230 /label= putative N-glycosylation site

FT Peptide 1..28 /label= transmembrane region

XX /label= signal peptide

PN EP417563-A.

XX 20-MAR-1991.

XX 31-AUG-1990; 90EP-0116707.

XX 20-APR-1990; 90CH-0001347.

PR 12-SEP-1989; 89CH-0003119.

PR 08-MAR-1990; 90CH-0000746.

XX (HOFF) HOFFMANN-LA ROCHE AG.

XX Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
 PI Schlaeager EJ;

XX WPI; 1991-081851/12.

DR N-PSDB; AAQ10955.

XX Insoluble tumour necrosis factor binding proteins - and DNA
 encoding them, useful in pharmaceutical prods. and for antibody
 prodn.

XX Claim 1; Fig 1; 26pp; German.

XX Partial amino acid sequences were determined for the 55 and 75kD
 CC TNF-BPs (see AAR11072-R11081) and oligonucleotide primers were
 CC synthesised based on these partial sequences. The primers were used
 CC to produce a cDNA fragment for use as a probe to screen a human
 CC placental cDNA bank constructed in lambda gt11. Positive clones were
 CC identified and sequenced. DNA constructs comprising the TNF-BP coding
 CC sequence may also contain a fragment encoding a human Ig domain.
 CC Recombinant constructs are used to transform cells to confer
 CC improved TNF-binding properties.
 CC See also AAQ10956.

XX Sequence 455 AA;

Query Match 99.0%; Score 1219; DB 12; Length 455;
 Best Local Similarity 100.0%; Pred. No. 2e-91;

Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLPHLGDRKDSVCPQGYIHPQNSICT 60
 DB 1 mglstvpdllplvlellvgyipsgviglphlgdrkrdsvcpqgyihpqnnsict 60

QY 61 KCHKGTLYLNDPCPGQDTCRECSGSFTASENHLRHLCSKCRKEMQVEISSCTVD 120
 DB 61 kchkgtlylndpcpgqgtdcrecsgsftasenhrlhrlcsckrkemqgveissctvd 120

QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQEKONTVCTCHAGFFLRNECV 180
 DB 121 rdtvcgcrknqyrhywsenlfqcfncslcngtvlhlsceqkntvctchagfflrenecv 180

QY 181 SCSCNCKKSLCTKCLPQIENVKGTEDSGTTVLLPLV 217
 DB 181 scsnckkslectkclpqienvkgtedsdgttvlplv 217

RESULT 5

AAR24000
 ID AAR24000 standard; Protein; 455 AA.

XX AC AAR24000;

DT 05-NOV-1992 (first entry)

XX TNF-alpha 55kD receptor.

XX tumour necrosis factor alpha; extracellular binding domain;
 KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
 KW malaria; viral meningitis; graft versus host disease;
 KW autoimmune disease; rheumatoid arthritis.

```
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..40
FT Modified-site /label= signal peptide
FT Modified-site 54..56
FT Modified-site /label= N linked glycosylation site
FT Modified-site /note= "potential"
FT Modified-site 145..147
FT Modified-site /label= N linked glycosylation site
FT Modified-site /note= "potential"
FT Modified-site 151..153
FT Modified-site /label= N linked glycosylation site
FT Modified-site /note= "potential"
FT Domain 212..234
FT /label= transmembrane domain
XX
XX WO9207076-A.
XX
XX 30-APR-1992.
XX
XX 18-OCT-1991; 91WO-GB01826.
XX
XX 18-OCT-1990; 90GB-0022648.
XX
XX (CHAR-) CHARING CROSS SUNLEY RES CENT.
XX
XX Brennan FM, Feldmann M, Gray PW, Turner MJC;
XX
XX WPI; 1992-167156/20.
XX N-PSDB; AAQ24440.
XX
XX New polypeptide capable of binding human TNF alpha - comprises
XX first three cysteine-rich subdomains of TNF alpha receptor for
XX treating autoimmune disease, septic shock, HIV etc.
XX
XX Example; Fig 1; 43pp; English.
XX
XX This sequence was deduced from human TNF-alpha cDNA isolated as in
XX AAQ24440. The first 35 amino acids are generally quite hydrophobic
XX and probably represent a signal sequence. Residues 35-40 are highly
XX charged (DREKR) and this is not normally found in secretory
XX signal sequences. It is possible the receptor is processed by
XX proteolysis after residue 40 which contains a dibasic cleavage site
XX (KR). Hydrophathy analysis of this sequence predicts a single
XX transmembrane domain of 23 amino acids, dividing the sequence into
XX an extracellular domain of 171 residues and a cytoplasmic domain of
XX 221 residues. The sequence contains a large number of cysteine
XX residues, the arrangement of which is similar to that of other cell
XX surface proteins, suggesting the TNF-alpha receptor is structurally
XX related to a family of receptors.
XX NOTE:- Residues 371,2 given in the sequence as T,L, are encoded by
XX TGG (W) and AAG (K).
XX See also AAQ24440-51, AAR24000, AAR24080-84, AAR27585, AAQ29236-8
XX Sequence 455 AA;
XX
XX Query Match 99.0%; Score 1219; DB 13; Length 455;
XX Best Local Similarity 100.0%; Pred. No. 2e-91;
XX Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 MGLSVNPDLPLVLELLVGYPSGVTGLVPHLGDREKRDVCPQKVIHPQNSICCT 60
XX Db 1 mgiscvdpdlplvlellvgypsgvtglvphlgdrekrdsvcpqkvihpqnsicct 60
XX
XX Qy 61 KCHKGTLYNDGPGQDTCRECSGSGFTASENHLRHLCSCKRKGQVEISCTVD 120
XX Db 61 kchkgtlyndcpggqdtcrecsgsftasenhrlhrlcsckrkengqveisctvd 120
XX
XX Qy 121 RDTVCGCRKNQYRHVWSNLFQCFNCISCLNCTVHLSQOEKQNTVCTCHAGFFLRENECV 180
XX Db 121 rdtvcgcrkngyrhvwslnfqcfncisclngtvhlscqekqntvctchagfflrenecv 180
XX
XX QY 181 SCSNCKSLECTKLCIPQIENVKGTEDSGTTVLLPLV 217
XX Db 181 scsnckkslectklcqpqienvkgtdsgttvllplv 217
XX
XX RESULT 6
XX AAR42059
XX ID AAR42059 standard; Protein; 455 AA.
XX XX
XX AC AAR42059;
XX XX
XX DT 29-APR-1994 (first entry)
XX XX
XX DE Lambda derived TNF-R.
XX XX
XX KW Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
XX KW IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
XX KW rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
XX KW pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
XX KW graft verses host disease; sepsis; inflammation; allergy;
XX KW autoimmune dysfunction.
XX XX
XX OS Homo sapiens.
XX OS Lambda-gt10-7ctnfbp.
XX XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..40
XX FT Protein /note= "Signal peptide"
XX FT 41..455
XX FT /note= "Mature hTNF-R"
XX
XX XX WO9319777-A.
XX PN
XX XX 14-OCT-1993.
XX PD
XX XX 26-MAR-1993; 93WO-US02938.
XX PF
XX XX 30-MAR-1992; 92US-0860710.
XX PR
XX XX (IMMV ) IMMUNEX CORP.
XX PA
XX XX Smith CA;
XX PI
XX XX WPI; 1993-336592/42.
XX DR N-PSDB; AAQ49932.
XX XX
XX PT New fusion protein tumour necrosis factor and human interleukin-1
XX PT receptor - useful in therapy, diagnosis and assays of e.g.
XX PT rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
XX
XX PS Disclosure; Page 57-59; 85pp; English.
XX
XX The sequences given in AAR42058-59 represent human tumour necrosis
XX factor receptor (TNF-R) and the sequences in AAR42060-61 represent
XX human interleukin-1 receptor (IL-1R). These sequences were used in
XX the production of a fusion protein which conformed to one of the
XX formulae:
XX TNF-R-linker-TNF-R-linker-IL-1R
XX IL-1R-linker-TNF-R-linker-TNF-R or
XX TNF-R-linker-TNF-R
XX
XX The linker may comprise 5-100 amino acids selected from Gly, Asp,
XX Ser, Thr and Ala. These linkers separate the individual moieties
XX by such a distance that each component of the fusion protein is
XX capable of folding into the secondary or tertiary structure required
XX for its biological activity. These fusion proteins may be used in
XX therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
XX particularly in conditions in which both TNF and IL-1 play a causative
XX role. They may be used to treat cachexia, rheumatoid arthritis,
XX diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
XX cerebral malaria, allograft and xenograft rejection in graft versus
XX host disease, sepsis, septic shock, inflammation, allergies and
XX autoimmune dysfunctions.
```

```
XX SQ Sequence 455 AA;
Query Match 99.0%; Score 1219; DB 14; Length 455;
Best Local Similarity 100.0%; Pred. No. 2e-91;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLLPLVLELLVIGPSGVLGPHLGRKRDSCVPGQKYIHPQNNISICT 60
DB 1 mglstvpdlllplvlellvlgpsvlgvphlgdrekrdsvcpqgkyihpqnnsict 60
QY 61 KCHKGTLYNDPCPGQDTRCECSGFTASENHLRHLCSCKRKEMGQVEISSCTVD 120
DB 61 kchkgtlyndpcpgqgdtrcecsgstasenhhlrhlscskrkemgqveissctvd 120
QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQEKQNTVCTCHAGFLRENECV 180
DB 121 rdtvcgcrknqyrhywsenlfqcfncslcngtvtvhlscqekqntvctchagflrenecv 180
QY 181 SCSCNCKSLECKLCPQIENVKGTEDSGTTVLLPLV 217
DB 181 scscnckslcklcpqienvkgtdsgttvllplv 217
RESULT 7
AAR75084
ID AAR75084 standard; Protein; 455 AA.
XX AC AAR75084;
XX DT 19-JAN-1996 (first entry)
XX DE p55 TNF-R.
XX KW p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;
XX KW epidermal growth factor receptor; EGF-R; protease; inhibitor;
XX KW phorbol myristate acetate; PMA.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Peptide 41..53
FT /note= "N terminus of soluble p55 TNF-R"
FT Modified-site 54..56
FT /note= "glycosylation site"
FT Modified-site 145..147
FT /note= "glycosylation site"
FT Modified-site 161..163
FT /note= "glycosylation site"
FT Peptide 193..210
FT /note= "peptide used in creation of chimeras"
FT Region 198..210
FT /note= "spacer region"
FT Misc-difference 201
FT /note= "major C terminus for soluble p55 TNF-R"
FT Misc-difference 202
FT /note= "essential for shedding reaction"
FT Misc-difference 203
FT /note= "minor C terminus for soluble p55 TNF-R"
FT Region 212..234
FT /note= "transmembrane region"
XX AU947542-A.
XX PN
XX PD
XX 04-MAY-1995.
XX 11-OCT-1994; 94AU-0075742.
XX 12-OCT-1993; 93IL-0107268.
XX (YEDA ) YEDA RES & DEV CO LTD.
```

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PI Batkin M, Brakebusch C, Varfolomeev E, Wallach D;
XX WPI; 1995-194342/26.
DR N-PSDB; AAQ90513.
XX New protease capable of cleaving soluble tumour necrosis factor
PT (TNF) receptor - from cell-bound TNF- receptor, useful for
PT antagonising deleterious effects of TNF.
XX Disclosure; Fig 1; 40pp; English.
XX This sequence represents human p55 tumour necrosis factor (TNF-R).
CC Expression of this receptor is regulated by shedding of the
CC extracellular receptor fragment. The p55 TNF-R can be shed in response
CC to different inducing agents, e.g. phorbol myristate acetate (PMA),
CC depending on cell type. The only region of the receptor whose structure
CC affects the shedding response is the spacer region (see AAR75012) in the
CC extracellular domain. This region is located close to a site of cleavage
CC of the molecule, and links the Cys rich module to the transmembrane
CC domain. The spacer region of the encoded protein was used to create the
CC chimeras between human p55 TNF-R and murine epidermal growth factor
CC receptor (EGF-R) that are represented by AAR75007-11. This spacer region
CC was subjected to deletion mutations (AAR75013-25) and substitutions
CC (AAR75026-47). Of the spacer region, the most important residues are
CC Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
CC important of these. The shedding of the receptor is independent of the
CC side chain identity of these residues, with the exception of a limited
CC dependence on the identity of Val 173. Mutations which alter the
CC conformation of the protein adversely effect the shedding process.
CC The mutations shown in AAR75013-47 were introduced in order to create an
CC inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC from the cell bound TNF-R. Fragments of these inhibitors can be seen in
CC AAR75017-9, AAR75025, AAR75033-5 and AAR75042-3. These protease
CC inhibitors can be used for enhancing TNF function.
XX SQ Sequence 455 AA;
Query Match 99.0%; Score 1219; DB 16; Length 455;
Best Local Similarity 100.0%; Pred. No. 2e-91;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLLPLVLELLVIGPSGVLGPHLGRKRDSCVPGQKYIHPQNNISICT 60
DB 1 mglstvpdlllplvlellvlgpsvlgvphlgdrekrdsvcpqgkyihpqnnsict 60
QY 61 KCHKGTLYNDPCPGQDTRCECSGFTASENHLRHLCSCKRKEMGQVEISSCTVD 120
DB 61 kchkgtlyndpcpgqgdtrcecsgstasenhhlrhlscskrkemgqveissctvd 120
QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQEKQNTVCTCHAGFLRENECV 180
DB 121 rdtvcgcrknqyrhywsenlfqcfncslcngtvtvhlscqekqntvctchagflrenecv 180
QY 181 SCSCNCKSLECKLCPQIENVKGTEDSGTTVLLPLV 217
DB 181 scscnckslcklcpqienvkgtdsgttvllplv 217
RESULT 8
AAY30934
ID AAY30934 standard; Protein; 455 AA.
XX AC AAY30934;
XX DT 18-OCT-1999 (first entry)
XX DE Human tumour necrosis factor binding protein.
XX KW Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;
XX KW anti-inflammatory; antimalarial; treatment; septic shock; inflammation;
XX KW autoimmune glomerulonephritis; cerebral malaria; immune response;
XX KW antagonist; diagnosis.
```

```
XX OS Homo sapiens.
XX EH Key Location/Qualifiers
XX FT Peptide 1..29
XX FT /label= signal_peptide
XX FT Protein 30..455
XX FT Modified-site 34
XX FT /note= "hypothetical glycosylation site"
XX FT Modified-site 125
XX FT /note= "hypothetical glycosylation site"
XX FT Modified-site 131
XX FT /note= "hypothetical glycosylation site"
XX FT Region 212..230
XX FT /note= "transmembrane region"
XX FT Modified-site 250
XX FT /note= "hypothetical glycosylation site"
XX PN EP939121-A2.
XX XX
XX PD 01-SEP-1999.
XX PF 31-AUG-1990; 90EP-0116707.
XX PR 20-APR-1990; 90CH-0001347.
XX PR 12-SEP-1989; 89CH-0003319.
XX PR 08-MAR-1990; 90CH-0000746.
XX PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
XX PI Schlaeger E;
XX DR WPI; 1999-480840/41.
XX DR N-PSDB; AAZ09170.
XX XX
XX PT New insoluble proteins, and fragments, that bind to tumor necrosis
XX PT factor, used to treat e.g. septic shock or cerebral malaria
XX PS Claim 4a; Fig 1; 25pp; German.
XX CC This invention describes novel homogeneous insoluble proteins (I),
XX CC their (in)soluble fragments (Ia) and their salts that can bind tumour
XX CC necrosis factor (TNF). The products of the invention have
XX CC anti-inflammatory and antimalarial activity. (I) and (Ia) are used (i)
XX CC to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
XX CC glomerulonephritis, cerebral malaria, immune responses and inflammation),
XX CC (ii) to purify TNF, (iii) to identify TNF (antagonists and (iv) for
XX CC diagnostic determination of TNF in body fluids. Antibodies raised against
XX CC (I) are used for affinity purification of (I). This sequence represents
XX CC a tumour necrosis factor binding protein described in the method of
XX CC the invention.
XX SQ Sequence 455 AA;
Query Match 99.0%; Score 1219; DB 20; Length 455;
Best Local Similarity 100.0%; Pred. No. 2e-91; Mismatches 0; Indels 0; Gaps 0;
Matches 217; Conservative 0;
QY 1 MGLSTVPDLLLVLELLVGIYPSGVIGLVPHLGDREKRDSCVCPQGYIHPQNNISCTCT 60
DB 1 mglstvpdlllplvlllellvgyipsgvlgvlphlgdrekrdscvcpqgyihpqnnsict 60
QY 61 KCHKGTLYNDCPGQDPTDCRECSGFTASENHLRHCLSCSKCKRKEMQGVSEISCTVD 120
DB 61 kchkgtlyndcpgqgdptdcrecsgstasenhhlrhclscskckrkemqgvseisctvd 120
QY 121 RDTVCGRKNQRYHWSNENLFCNCSLCLNGTVHLSQEKQNTVCTCHAGFFLRENECV 180
DB 121 rdtvcgrknqryhwsenlfcncslclngtvhlscqekqntvctchagfflrenecev 180
QY 181 SCSNCKKSLCTKLCPLQIENVKGTEDSGTTVLLPLV 217
```

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DB 181 scsnckkslectklclpqienvkgtedsgttvllplv 217
RESULT 9
AAB36266
ID AAB36266 standard; Protein; 455 AA.
XX AAB36266;
AC AAB36266;
XX XX
XX DT 20-FEB-2001 (first entry)
XX DE Human tumour necrosis factor receptor 1.
XX KW Human; death domain containing receptor; DR3-V1; cancer;
XX KW autoimmune disorder; inflammation; cardiovascular disorder; infection;
XX KW neurodegenerative disease; angiogenesis.
XX OS Homo sapiens.
XX PN WO200064465-A1.
XX PD 02-NOV-2000.
XX PF 21-APR-2000; 2000WO-US10741.
XX PR 22-APR-1999; 99US-0130488.
XX PR 28-MAY-1999; 99US-0136741.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (UNMI) UNIV MICHIGAN.
XX PA (YUGG/) YU G.
XX PA (NIJJ/) NI J.
XX PA (GENT/) GENTZ R L.
XX PA (DILL/) DILLON P J.
XX PA (DIXI/) DIXIT V M.
XX PI Yu G, Ni J, Gentz RL, Dillon PJ, Dixit VM;
XX WPI; 2000-687263/67.
XX PT Treating graft-versus-host disease, cancer, immunodeficiency or an
XX PT autoimmune disease comprising administering an antibody to Death Domain
XX PT Containing Receptor proteins and a second therapeutic agent -
XX PS Disclosure; Fig 3; 273pp; English.
XX CC The present invention provides the protein and coding sequences for two
XX CC death domain containing receptors, designated DR3 and DR3-V1. These
XX CC receptors are involved in apoptosis, and the sequences given can be used
XX CC in the treatment of cancers, infections, cardiovascular disorders such as
XX CC arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms
XX CC and congenital heart defects, neurodegenerative diseases including
XX CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
XX CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
XX CC and to promote angiogenesis and wound healing.
XX SQ Sequence 455 AA;
Query Match 99.0%; Score 1219; DB 21; Length 455;
Best Local Similarity 100.0%; Pred. No. 2e-91;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLLVLELLVGIYPSGVIGLVPHLGDREKRDSCVCPQGYIHPQNNISCTCT 60
DB 1 mglstvpdlllplvlllellvgyipsgvlgvlphlgdrekrdscvcpqgyihpqnnsict 60
QY 61 KCHKGTLYNDCPGQDPTDCRECSGFTASENHLRHCLSCSKCKRKEMQGVSEISCTVD 120
DB 61 kchkgtlyndcpgqgdptdcrecsgstasenhhlrhclscskckrkemqgvseisctvd 120
QY 121 RDTVCGRKNQRYHWSNENLFCNCSLCLNGTVHLSQEKQNTVCTCHAGFFLRENECV 180
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Db 121 rdtvcgrknqyrhysenlfqcfncslclngtvtvhlscqekqntvctchagfflrenecev 180
QY 181 SCSCNCKSLECTKLCPLQIENVKGTEDSGTFTVLLPLV 217
Db 181 scsnckselectkclcpqienkvgtedsgttvllplv 217
RESULT 10
AAB37800
ID AAB37800 standard; Protein: 455 AA.
XX
AC AAB37800;
XX
DT 23-FEB-2001 (first entry)
XX
DE Human tumour necrosis factor p55 receptor.
XX
KW Human; tumour necrosis factor; TNF; TNF-alpha; TNF-beta; p55 receptor;
KW p75 receptor; antiinflammatory; haemostatic; antibacterial; sepsis;
KW immunosuppressive; immunomodulator; cardiant; cytostatic; cachexia;
KW neuroprotective; respiratory; inflammation; infection; Crohn's disease;
KW multiple sclerosis; autoimmune disorder; cardiovascular disorder;
KW chronic myelogenous leukaemia; inflammatory bowel disease.
XX
OS Homo sapiens.
XX
PN WO200064479-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-US11700.
XX
PR 27-APR-1999; 99US-0301274.
XX
PA (ANTI-) ANTIBODY SYSTEMS INC.
XX
PI Fredeking TM, Ignatyev GM;
XX
DR WPI: 2000-679646/56.
XX
PT Novel compositions comprising tetracycline or tetracycline-like
PT compounds for the treatment and/or prevention of acute inflammatory
PT responses and diseases, e.g. septic shock and immune complex-induced
PT colitis -
XX
PS Disclosure: Page 167-169; 183pp; English.
XX
CC The present sequence is given in a specification relating to novel
CC compositions and methods containing tetracycline or tetracycline-like
CC compounds for treating and/or preventing acute inflammatory responses and
CC diseases. Such diseases include acute inflammatory conditions associated
CC with viral haemorrhagic diseases (including diseases caused by
CC Bunyaviridae, Filoviridae, Flaviviridae or Arenaviridae viruses),
CC parasitic diseases, bacterial infections, sepsis, cachexia, autoimmune
CC disorders, acute cardiovascular events, chronic myelogenous leukaemia and
CC transplanted bone marrow-induced graft-versus-host disease, septic shock,
CC immune complex-induced colitis, cerebrospinal fluid inflammation,
CC multiple sclerosis, inflammatory responses associated with trauma,
CC systemic inflammatory response syndrome (SIRS), adult respiratory
CC distress syndrome (ARDS), acute liver failure, inflammatory bowel disease
CC and Crohn's disease.
XX
SQ Sequence 455 AA;

Query Match 99.0%; Score 1219; DB 21; Length 455;
Best Local Similarity 100.0%; Pred. No. 2e-91; Indels 0; Gaps 0;
Matches 217; Conservative 0; Mismatches 0;

QY 1 MGLSTVPDLLPLVLELVGIVPSGVIGLPHLGREKRDSCVPGQKYTHPQNNSICCT 60
Db 1 mglstvpdllplvllvllvlgivpsgviglpblgdrkrdscvpgqkythpqnnsicct 60

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QY 61 KCHKGTLYLNDPCPGQDTDCRECSGSFTASENHLRHLCSCKRKMGGQVEISSCTVD 120
Db 61 kchkgtlylndpcpgqdtcrecsgsftasenhrlhclscskcrkemgqvveissctvd 120
QY 121 RDTVCGCRKNQYRHWSENLFQCFNCSLCLNGTHTVHLSQEKQNTVCTCHAGFFLRENECV 180
Db 121 rdtvcgrknqyrhysenlfqcfncslclngtvtvhlscqekqntvctchagfflrenecev 180
QY 181 SCSCNCKSLECTKLCPLQIENVKGTEDSGTFTVLLPLV 217
Db 181 scsnckselectkclcpqienkvgtedsgttvllplv 217

```

RESULT 11

AAB26984
ID AAB26984 standard; Protein: 455 AA.

XX AAB26984;

XX 02-FEB-2001 (first entry)

XX Human TNFR 1.

DE Human TNFR 1.
XX Human; TNFR 1; tumour necrosis factor; TR9 receptor; immunosuppressive;
KW antiinflammatory; cardiant; antiasthmatic; antidiabetic; antiallergic;
KW antiarthritic; antirheumatic; anti-HIV; anticonvulsant; cytostatic;
KW neuroprotective; gene therapy; Death Domain Containing Receptor 6;
KW common variable immunodeficiency; X-linked agammaglobulinaemia;
KW severe combined immunodeficiency; Wiskott-Aldrich syndrome;
KW autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis;
KW multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer;
KW cardiovascular disease; neurological disease; protein coordinate data.

XX Homo sapiens.

OS WO200056862-A1.

XX 28-SEP-2000.

XX 16-MAR-2000; 2000WO-US06831.

XX 24-MAR-1999; 99US-0126019.

XX 14-MAY-1999; 99US-0134220.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ni J, Gentz RL, Yu G, Fan P;

XX WPI: 2000-594575/56.

XX Nucleic acid molecule encoding a human tumor necrosis factor receptor,
PT known as TR9, useful for treating, preventing and diagnosing severe
PT combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy
PT and cancer -

XX Disclosure: Fig 2; 220pp; English.

XX The present sequence is TNFR 1, a member of the tumour necrosis factor
CC receptor family. A novel human tumour necrosis factor receptor,
CC designated TR9, has been isolated. The TR9 receptor is also known as
CC Death Domain Containing Receptor 6. TR9 polypeptides, polynucleotides or
CC agonists are useful for treating, preventing or diagnosing common
CC variable immunodeficiency, X-linked agammaglobulinaemia, severe combined
CC immunodeficiency and Wiskott-Aldrich syndrome, autoimmune diseases (such
CC as rheumatoid arthritis, allergic encephalomyelitis, multiple sclerosis,
CC diabetes mellitus and asthma), HIV infection, epilepsy, cancer,
CC cardiovascular diseases and other neurological diseases.

XX Sequence 455 AA;

Query Match 99.0%; Score 1219; DB 21; Length 455;

Best Local Similarity 100.08; Pred. No. 2e-91; Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLLVLELLVGIYPSGVLPHLGDREKRDVCPQGYIHPQNNISICT 60
DB 1 mglstvpdlllvlellvgiypsgvlphlgdrekrdsvcpqgyihpqnnsicct 60

QY 61 KCHKGTLYNDPCPGQDPTDCRECSGSFTASENHLRHLCSCKRKGQVEISSCTVD 120
DB 61 kchkgtlyndcpgpgqdtcrecesgsftasenhrlhclscskcrkemgqveissctvd 120

QY 121 RDTVCGRKNQRYHWSNLFQCFNCSLCLNGTVHLSCEKQNTVCTCHAGFFLRENECV 180
DB 121 rdtvcgrknqryhwsenlfqcfncslclngtvhlscqekqntvctchagfflrenevcv 180

QY 181 SCNCKKSLECTKLCPLQIENVKGTEDSGTTVLLPLV 217
DB 181 scnckkslectklcplqienvkgtdsgttvllplv 217

RESULT 12
AAB23446
ID AAB23446 standard; Protein; 455 AA.
XX AAB23446;
AC AAB23446;
DT 12-JAN-2001 (first entry)
DE Human tumour necrosis factor receptor 1 protein.
XX TNFR1; tumour necrosis factor receptor; polymorphism; human;
KW tumour; cancer; apoptosis; bacterial infection.
XX Homo sapiens.
XX WO200050436-A1.
XX 31-AUG-2000.
XX 23-FEB-2000; 2000WO-US04606.
XX 23-FEB-1999; 99US-0121314.
XX (GENA-) GENAISSANCE PHARM INC.
XX (NAND/) NANDABALAN K.
XX (SCHU/) SCHULZ V P.
XX (STEP/) STEPHENS J C.
XX (CHEW/) CHEW A.
XX Nandabalan K, Schulz VP, Stephens JC, Chew A;
XX WPI; 2000-543909/49.
XX N-PSDB; AAA95105.
XX Polynucleotides comprising polymorphic variants of a reference sequence for tumour necrosis factor receptor 1 (TNFR1), useful for studying the biological function of TNFR1 and identifying drugs targeting the protein for treating disorders -
XX Claim 10; Fig 5; 79pp; English.
XX The present invention relates to polymorphic variants of the tumour necrosis factor receptor 1 (TNFR1) gene. The present sequence is the TNFR1 protein. The sequence of the whole gene is given in AAA95102, CC AAA95103 and AAA95104. The polymorphisms were identified by amplifying CC and sequencing regions of the gene. Twelve polymorphic loci CC were discovered. Of these twelve polymorphisms, four can cause a CC change in the TNFR1 protein. The TNFR1 polymorphisms may be useful CC for studying the biological function of TNFR1 as well as for CC identifying drugs targeting the protein for treatment of disorders CC related to its abnormal expression or function such as tumours, CC apoptosis related disorders and bacterial infection.
XX

SQ Sequence 455 AA;

Query Match 99.0%; Score 1219; DB 21; Length 455;
Best Local Similarity 100.0%; Pred. No. 2e-91; Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLLVLELLVGIYPSGVLPHLGDREKRDVCPQGYIHPQNNISICT 60
DB 1 mglstvpdlllvlellvgiypsgvlphlgdrekrdsvcpqgyihpqnnsicct 60

QY 61 KCHKGTLYNDPCPGQDPTDCRECSGSFTASENHLRHLCSCKRKGQVEISSCTVD 120
DB 61 kchkgtlyndcpgpgqdtcrecesgsftasenhrlhclscskcrkemgqveissctvd 120

QY 121 RDTVCGRKNQRYHWSNLFQCFNCSLCLNGTVHLSCEKQNTVCTCHAGFFLRENECV 180
DB 121 rdtvcgrknqryhwsenlfqcfncslclngtvhlscqekqntvctchagfflrenevcv 180

QY 181 SCNCKKSLECTKLCPLQIENVKGTEDSGTTVLLPLV 217
DB 181 scnckkslectklcplqienvkgtdsgttvllplv 217

RESULT 13
AAB01336
ID AAB01336 standard; Protein; 455 AA.
XX AAB01336;
AC AAB01336;
DT 25-SEP-2000 (first entry)
DE TNF-R1 death receptor.
XX ULL144; death receptor; apoptosis; programmed cell death; FAS;
KW TNF-R1; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;
KW human.
XX Homo sapiens.
XX WO200034335-A2.
XX 15-JUN-2000.
XX 03-DEC-1999; 99WO-US26035.
XX 04-DEC-1998; 98US-0205018.
XX (SCHE) SCHERING CORP.
XX Leong C, Phillips JH;
XX WPI; 2000-423383/36.
XX Purified or recombinant polypeptide for modulating apoptosis comprises a sequence which binds to an antibody specific for ULL144 or its fragments
XX Disclosure; Page 65-67; 76pp; English.
XX A pure or recombinant polypeptide which binds to a polyclonal antibody specific for the mature ULL144 is useful for screening molecules which block induction of apoptosis or interfere with antiapoptotic activity. The polypeptide is also useful for modulating apoptosis and useful in treatment of conditions associated with abnormal physiology or development, such as cancer or degenerative conditions and for regulation of viral infection and replication. At least five different death receptors are known, which include the CD95 (fas/APO-1), the TNF receptor-1, TNF receptor apoptosis-mediated protein (TRAMP), death receptor-6 (DR-6), and TNF-related apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.
XX Sequence 455 AA;

CC parasite, bacteria and viruses, restenosis and graft versus host disease. CC They are also useful for inducing proliferation of T-cells, endothelial CC cells and certain haematopoietic cells, to regulate antiviral responses CC and to prevent certain autoimmune diseases after stimulation of TR1D by CC an agonist or TRAIL binding facilitator. The antibodies which bind TR1D CC polypeptides are useful for treating and/or preventing diseases CC associated with increased or decreased apoptotic cell death. The TR1D CC polynucleotides, proteins, antibodies, agonists and antagonists are CC useful in the diagnosis, treatment or prevention of: (a) cancer; CC (b) autoimmune disorders; (c) diseases associated with increased CC apoptosis; (d) cardiovascular disorders; and (e) viral infection. The CC present sequence represents a tumour necrosis factor receptor used in CC comparison with TR1D in the exemplification of the present invention. CC XX

Seq Sequence 455 AA;

Query Match 99.0%; Score 1219; DB 22; Length 455;
Best Local Similarity 100.0%; Pred. No. 2e-91;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSTVPDLLPLVLELLVGYPSGVIGLVPHLGDRKDSVCPQGRYIHPPNNSICT 60
Db 1 mglstvpdllplvllellvgypsgviglvphlgdrekdrsvcpqgkyihppnnsicct 60

Qy 61 KKHGTYLYNDPCPGQDTCRECESSGFTASENHLRHLCSCKRKGVEISSCTVD 120
Db 61 kkhgtylyndpcpgqgtdcrecesgsftasenhhlrhlscskrkemgqveissctvd 120

Qy 121 RDTVCGCRKNQYRHWSENLFQCFNCSLCINGTVHLSCEQKQNTVCTCHAGFFLRENECV 180
Db 121 rdtvcgrkndyrhwsenlfcfnscslcngtvhlscqekqntvctchagfflrenevcv 180

Qy 181 SCSCNCKSLECTKCLPOIENVKGTEDSGTTVLLPLV 217
Db 181 scscnckselectkclclpqienvkgtedsgttvllplv 217

RESULT 15
ID AAB37677 standard; protein; 455 AA.
XX AAB37677;
AC AAB37677;
DT 02-MAR-2001 (first entry)
XX Human 30 kDa TNF inhibitor precursor.
DE
XX TNF inhibitor; antinflammatory; Tumour Necrosis Factor; Interleukin;
KW IL-1; inflammatory disease; degenerative disease; human.
XX
XX Homo sapiens.
OS
XX
XX US6143866-A.
XX
XX 07-NOV-2000.
XX
XX 19-JAN-1995; 95US-0375242.
XX
XX 19-JUL-1993; 90US-0555274.
PR 09-JUL-1993; 93US-0090366.
PR 18-JUL-1989; 89US-0381080.
PR 11-DEC-1989; 89US-0450329.
PR 07-FEB-1990; 90US-0479661.
XX
XX (AMGE-) AMGEN INC.
XX
XX Squires C, King MW, Hale KK, Brewer MT, Thompson RC;
PI Vanderslice RW, Vannice J, Kohno T;
XX
XX WPI; 2001-006443/01.
DR
DR N-PSDB; AAC83946.
XX

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2001, 05:31:58 ; Search time 13.45 Seconds
(without alignments)
335.263 Million cell updates/sec

Title: US-09-599-400A-9
Perfect score: 1231
Sequence: 1 MGLSTVPDLLPLVLLLELV.....ENKGTEDSGTIVLLPLVRP 219

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1219	99.0	280	3	US-08-974-022-46
2	1219	99.0	455	1	US-08-050-319B-25
3	1219	99.0	455	1	US-08-321-668-2
4	1219	99.0	455	1	US-08-837-941-2
5	1219	99.0	455	2	US-08-126-016-2
6	1219	99.0	455	2	US-08-465-982-25
7	1219	99.0	455	4	US-08-815-469-5
8	1189	96.6	453	4	US-09-086-483A-5
9	1124	91.3	199	1	US-08-050-319B-48
10	1124	91.3	199	2	US-08-465-982-48
11	992.5	80.6	336	4	US-08-804-166-8
12	992.5	80.6	336	4	US-08-910-991-8
13	979	79.5	285	4	US-08-804-166-6
14	979	79.5	285	4	US-08-910-991-6
15	946	76.8	167	1	US-08-050-319B-2
16	946	76.8	167	1	US-08-050-319B-57
17	946	76.8	167	2	US-08-465-982-2
18	946	76.8	167	2	US-08-465-982-57
19	900	73.1	153	2	US-08-219-237B-4
20	900	73.1	153	4	US-08-477-347-12
21	873	70.9	154	2	US-08-232-087A-10
22	854.5	69.4	158	1	US-08-050-319B-54
23	854.5	69.4	158	2	US-08-465-982-54
24	842.5	68.4	256	4	US-08-804-166-2
25	842.5	68.4	256	4	US-08-910-991-2
26	840	68.2	153	1	US-08-050-319B-52
27	840	68.2	153	2	US-08-465-982-52

28	840	68.2	157	1	US-08-050-319B-50
29	840	68.2	157	2	US-08-465-982-50
30	837	68.0	307	4	US-08-804-166-4
31	837	68.0	307	4	US-08-910-991-4
32	731	59.4	124	1	US-08-050-319B-4
33	731	59.4	124	2	US-08-465-982-4
34	357	29.0	62	3	US-08-904-446A-17
35	249	20.2	40	1	US-08-050-319B-26
36	249	20.2	40	2	US-08-465-982-26
37	245	19.9	41	1	US-08-050-319B-36
38	245	19.9	41	2	US-08-465-982-36
39	237	19.3	43	1	US-08-050-319B-31
40	237	19.3	43	2	US-08-465-982-31
41	220	17.9	39	1	US-08-050-319B-40
42	220	17.9	39	2	US-08-465-982-40
43	216.5	17.6	428	4	US-08-815-469-2
44	210.5	17.1	197	2	US-08-505-606-1
45	208	16.9	417	4	US-08-815-469-4

ALIGNMENTS

RESULT 1
US-08-974-022-46
; Sequence 46, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPEPTIDE
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-022-46

Query Match 99.0%; Score 1219; DB 3; Length 280;
Best Local Similarity 100.0%; Pred.No. 1.2e-101;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLPLVLLLELVGIVPSGVIGLPHLDREKRSVCPQGYIHPQNNISICT 60
DB 1 MGLSTVPDLLPLVLLLELVGIVPSGVIGLPHLDREKRSVCPQGYIHPQNNISICT 60

QY 61 KCHKTYLYNDPCPGQDTCRECSGSGFTASENHLRHCLSCSKCKRMKGQVEISSCTVD 120
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Db 61 KCHKTYLYNDPCPGQDTCRECSGSGFTASENHLRHCLSCSKCKRMKGQVEISSCTVD 120
|||||
QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180
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Db 121 RDTVCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180
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QY 181 SC SNCKKSLECTKLCPLQIENVKGTEDSGTTVLLPLV 217
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Db 181 SC SNCKKSLECTKLCPLQIENVKGTEDSGTTVLLPLV 217
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RESULT 2
US-050-319B-25
; Sequence 25, Application US/08050319B
; Patent No. 5633145
; GENERAL INFORMATION:
; APPLICANT: M. Feldmann, P.W. Gray,
; APPLICANT: M.J.C. Turner, F.M. Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050.319B
; FILING DATE: 10-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-050-319B-25
Query Match 99.0%; Score 1219; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 2.le-101;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLLPLVLELLVGIYPSGVIGLVPHLGDREKRDSDVCPQGYIHPQNNISICT 60
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Db 1 MGLSTVPDLLLPLVLELLVGIYPSGVIGLVPHLGDREKRDSDVCPQGYIHPQNNISICT 60
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QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180
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Db 121 RDTVCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180
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QY 181 SC SNCKKSLECTKLCPLQIENVKGTEDSGTTVLLPLV 217
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Db 181 SC SNCKKSLECTKLCPLQIENVKGTEDSGTTVLLPLV 217
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Db 181 SC SNCKKSLECTKLCPLQIENVKGTEDSGTTVLLPLV 217
|||||
RESULT 3
US-08-321-668-2
; Sequence 2, Application US/08321668
; Patent No. 5665859
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; APPLICANT: VARFOLOMEEV, Eugene
; APPLICANT: BATKIN, Michael
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/321,668
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107268
; FILING DATE: 12-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-321-668-2
Query Match 99.0%; Score 1219; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 2.le-101;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLLPLVLELLVGIYPSGVIGLVPHLGDREKRDSDVCPQGYIHPQNNISICT 60
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Db 1 MGLSTVPDLLLPLVLELLVGIYPSGVIGLVPHLGDREKRDSDVCPQGYIHPQNNISICT 60
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|||||
Db 61 KCHKTYLYNDPCPGQDTCRECSGSGFTASENHLRHCLSCSKCKRMKGQVEISSCTVD 120
|||||
QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180
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Db 121 RDTVCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180
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QY 181 SC SNCKKSLECTKLCPLQIENVKGTEDSGTTVLLPLV 217
|||||
Db 181 SC SNCKKSLECTKLCPLQIENVKGTEDSGTTVLLPLV 217
|||||

GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,982
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319
FILING DATE: 10-May-1993
ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-982-25

Query Match 99.0%; Score 1219; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 2.1e-101;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLLPLVLELLVGIYPSGVIGLPHLGDREKRDVCPQGYIHPQNNISICT 60
DB 1 MGLSTVPDLLLPLVLELLVGIYPSGVIGLPHLGDREKRDVCPQGYIHPQNNISICT 60
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DB 121 RDTVCGCRKNQRYHWSNLFQCFNCSLCLNGTVHLSQEKQNTVCTCHAGFFLRENECV 180
QY 181 SCSNCKKSLCTKLCPLQIENVKGTEDSGTTVLLPLV 217
DB 181 SCSNCKKSLCTKLCPLQIENVKGTEDSGTTVLLPLV 217

RESULT 7
US-08-465-982-25
Sequence 5, Application US/08815469
Patent No. 6153402
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors

NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 6153402 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-815-469-5

Query Match 99.0%; Score 1219; DB 4; Length 455;
Best Local Similarity 100.0%; Pred. No. 2.1e-101;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLLPLVLELLVGIYPSGVIGLPHLGDREKRDVCPQGYIHPQNNISICT 60
DB 1 MGLSTVPDLLLPLVLELLVGIYPSGVIGLPHLGDREKRDVCPQGYIHPQNNISICT 60
QY 61 KCHKGTLYNDPCPGQDTCRECSGSFTASENHLRHLCLSCSKCKRMKGQVEISSCTVD 120
DB 61 KCHKGTLYNDPCPGQDTCRECSGSFTASENHLRHLCLSCSKCKRMKGQVEISSCTVD 120
QY 121 RDTVCGCRKNQRYHWSNLFQCFNCSLCLNGTVHLSQEKQNTVCTCHAGFFLRENECV 180
DB 121 RDTVCGCRKNQRYHWSNLFQCFNCSLCLNGTVHLSQEKQNTVCTCHAGFFLRENECV 180
QY 181 SCSNCKKSLCTKLCPLQIENVKGTEDSGTTVLLPLV 217
DB 181 SCSNCKKSLCTKLCPLQIENVKGTEDSGTTVLLPLV 217

RESULT 8
US-09-086-483A-5
Sequence 5, Application US/09086483A
Patent No. 6214580
GENERAL INFORMATION:
APPLICANT: NI, et al.
TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/086,483A
FILING DATE: May-29-98

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/050,936

FILING DATE: May-30-97

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/069,112

FILING DATE: Dec-9-97

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BROOKES, ANDERS A.

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PF379

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 453 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-086-483A-5

Query Match 96.6%; Score 1189; DB 4; Length 453;

Best Local Similarity 99.1%; Pred. No. 9.9e-99;

Matches 215; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHPQNNISICT 60

Db 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHPQNNISICT 58

QY 61 KCHKGTLYNDPCPGQDTCRECSGSFTASENHLRHLCSCKRKGQVEISSCTVD 120

Db 59 KCHKGTLYNDPCPGQDTCRECSGSFTASENHLRHLCSCKRKGQVEISSCTVD 118

QY 121 RDTVCGCRKNQRYHWSLENLFCFNCISLCLNGTVHLSQCEKQNTVCTCHAGFFLRENECV 180

Db 119 RDTVCGCRKNQRYHWSLENLFCFNCISLCLNGTVHLSQCEKQNTVCTCHAGFFLRENECV 178

QY 181 SCSCNCKSLECKLCLPQIENVKGTEDSGTTLPLV 217

Db 179 SCSCNCKSLECKLCLPQIENVKGTEDSGTTLPLV 215

RESULT 9

US-08-050-319B-48

Sequence 48, Application US/08050319B

Patent No. 5633145

GENERAL INFORMATION:

APPLICANT: M.Feldmann, P.W. Gray,

APPLICANT: M.J.C. Turner, F.M. Brennan

TITLE OF INVENTION: Modified human TNFalpha (Tumor

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Reed & Robbins

STREET: 635 Bryant Street

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/050,319B

FILING DATE: 10-May-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Robbins, Roberta L.

REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 5150-0030

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 617-8999

TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 199 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-050-319B-48

Query Match 91.3%; Score 1124; DB 1; Length 199;

Best Local Similarity 99.5%; Pred. No. 2.6e-93;

Matches 198; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHPQNNISICT 60

Db 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHPQNNISICT 60

QY 61 KCHKGTLYNDPCPGQDTCRECSGSFTASENHLRHLCSCKRKGQVEISSCTVD 120

Db 61 KCHKGTLYNDPCPGQDTCRECSGSFTASENHLRHLCSCKRKGQVEISSCTVD 120

QY 121 RDTVCGCRKNQRYHWSLENLFCFNCISLCLNGTVHLSQCEKQNTVCTCHAGFFLRENECV 180

Db 121 RDTVCGCRKNQRYHWSLENLFCFNCISLCLNGTVHLSQCEKQNTVCTCHAGFFLRENECV 180

QY 181 SCSCNCKSLECKLCLPQI 199

Db 181 SCSCNCKSLECKLCLPQI 199

RESULT 10

US-08-465-982-48

Sequence 48, Application US/08465982

Patent No. 5863786

GENERAL INFORMATION:

APPLICANT: M.Feldmann, P.W. Gray,

APPLICANT: M.J.C. Turner, F.M. Brennan

TITLE OF INVENTION: Modified human TNFalpha (Tumor

TITLE OF INVENTION: Necrosis Factor alpha) Receptor

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Reed & Robbins

STREET: 635 Bryant Street

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, version #1.25

;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/465,982
;/ FILING DATE:
;/ CLASSIFICATION:
;/ PRIOR APPLICATION DATA: US/08/050,319
;/ FILING DATE: 10-May-1993
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Robbins, Robert L.
;/ REGISTRATION NUMBER: 33,208
;/ REFERENCE/DOCKET NUMBER: 5150-0030
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (415) 617-8999
;/ TELEFAX: (415) 327-3231
;/ INFORMATION FOR SEQ ID NO: 48:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 199 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ US-08-465-982-48

Query Match 91.3%; Score 1124; DB 2; Length 199;
Best Local Similarity 99.5%; Pred. No. 2.6e-93;
Matches 198; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLLPLVLELVGYPGIVGLPHLGDREKRDVCPGKGYTHPQNNSTCT 60
Db 1 MGLSTVPDLLLPLVLELVGYPGIVGLPHLGDREKRDVCPGKGYTHPQNNSTCT 60
QY 61 KCHKGTYLNDPCPGQDTCRECESSFTASENHLRHCLSCSKCRKEMQVEISSCTVD 120
Db 61 KCHKGTYLNDPCPGQDTCRECESSFTASENHLRHCLSCSKCRKEMQVEISSCTVD 120
QY 121 RTVCGCRKNQRYHWSENLFCQFNCSLCLNGTVHLSQCKQNTVCTCHAGFFLRENECV 180
Db 121 RTVCGCRKNQRYHWSENLFCQFNCSLCLNGTVHLSQCKQNTVCTCHAGFFLRENECV 180
QY 181 SCSNCKKSLECTKCLPQI 199
Db 181 SCSNCKKSLECTKCLPQI 199

RESULT 11
US-08-166-8
; Sequence 8, Application US/08804166
; Patent No. 6193972
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,166
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/011,936
; FILING DATE: 20 February 1996

;/ CLASSIFICATION:
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Browdy, Roger L.
;/ REGISTRATION NUMBER: 25,618
;/ REFERENCE/DOCKET NUMBER: CAMPBELL-2A
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (202) 628-5197
;/ TELEFAX: (202) 737-3528
;/ INFORMATION FOR SEQ ID NO: 8:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 336 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ US-08-804-166-8
Query Match 80.6%; Score 992.5; DB 4; Length 336;
Best Local Similarity 96.7%; Pred. No. 2.4e-81;
Matches 174; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 41 DSVCPQKGYTHPQNNSTCTCKCHKGYLYNDPCPGQDTCRECESSFTASENHLRHCL 100
Db 23 DSVCPQKGYTHPQNNSTCTCKCHKGYLYNDPCPGQDTCRECESSFTASENHLRHCL 82
QY 101 SCSKCRKEMQVEISSCTVDRTVCGCRKNQRYHWSENLFCQFNCSLCLNGTVHLSQCE 160
Db 83 SCSKCRKEMQVEISSCTVDRTVCGCRKNQRYHWSENLFCQFNCSLCLNGTVHLSQCE 142
QY 161 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKCLPQIENVKGTEDSGTTV-LPLVPR 219
Db 143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKCLPQIENVKGTEDSGTTAGAGPRCRP 202
RESULT 12
US-08-910-991-8
; Sequence 8, Application US/08910991
; Patent No. 6194177
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,991
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/804,166
; FILING DATE: 20 February 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/011,936
; FILING DATE: 20 February 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: CAMPBELL-2B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-910-991-8

Query Match 80.6%; Score 992.5; DB 4; Length 336;
Best Local Similarity 96.7%; Pred. No. 2.4e-81;
Matches 174; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 41 DSVCPQGYIHPQNNISICCTKCHKGTLYLNDPCPGQDQTDRCESGFTASENHLRHCL 100
DB 23 DSVCPQGYIHPQNNISICCTKCHKGTLYLNDPCPGQDQTDRCESGFTASENHLRHCL 82
QY 101 SCSKCRKEMGOVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSQOE 160
DB 83 SCSKCRKEMGOVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSQOE 142
QY 161 KONTVCTCHAGFFLRENECVSCNCKSLECTKLCPLQIENVKGTEGTTV-LLPLVRP 219
DB 143 KONTVCTCHAGFFLRENECVSCNCKSLECTKLCPLQIENVKGTEGTTAGAGPCR 202

RESULT 13

US-08-804-166-6
Sequence 6, Application US/08804166
Patent No. 6193972
GENERAL INFORMATION:
APPLICANT: Campbell, Robert K.
APPLICANT: Jameson, Bradford A.
APPLICANT: Chappel, Scott C.
TITLE OF INVENTION: HYBRID PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 22207
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,166
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011,936
FILING DATE: 20 February 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: CAMPBELL-2A
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-804-166-6

Query Match 79.5%; Score 979; DB 4; Length 285;

Best Local Similarity 98.8%; Pred. No. 3.3e-80;
Matches 169; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 41 DSVCPQGYIHPQNNISICCTKCHKGTLYLNDPCPGQDQTDRCESGFTASENHLRHCL 100
DB 23 DSVCPQGYIHPQNNISICCTKCHKGTLYLNDPCPGQDQTDRCESGFTASENHLRHCL 82
QY 101 SCSKCRKEMGOVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSQOE 160
DB 83 SCSKCRKEMGOVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSQOE 142
QY 161 KONTVCTCHAGFFLRENECVSCNCKSLECTKLCPLQIENVKGTEGTT 211
DB 143 KONTVCTCHAGFFLRENECVSCNCKSLECTKLCPLQIENVKGTEGTT 193

RESULT 14

US-08-910-991-6
Sequence 6, Application US/08910991
Patent No. 6194177
GENERAL INFORMATION:
APPLICANT: Campbell, Robert K.
APPLICANT: Jameson, Bradford A.
APPLICANT: Chappel, Scott C.
TITLE OF INVENTION: HYBRID PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 22207
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,991
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/804,166
FILING DATE: 20 February 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011,936
FILING DATE: 20 February 1996
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: CAMPBELL-2B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-910-991-6

Query Match 79.5%; Score 979; DB 4; Length 285;

Best Local Similarity 98.8%; Pred. No. 3.3e-80;
Matches 169; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 41 DSVCPQGYIHPQNNISICCTKCHKGTLYLNDPCPGQDQTDRCESGFTASENHLRHCL 100
DB 23 DSVCPQGYIHPQNNISICCTKCHKGTLYLNDPCPGQDQTDRCESGFTASENHLRHCL 82
QY 101 SCSKCRKEMGOVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSQOE 160

Db 83 SCSCRKEMGQVEISSCTVDRVTGCGCRKNQRYHYWSENLFQCFNCTCLNGTVHLSCOE 142
QY 161 KQNTVCTCHAGFFLENECVSCSNCKKSLCKLCLPQIENVKGTEDSGTT 211
Db 143 KQNTVCTCHAGFFLENECVSCSNCKKSLCKLCLPQIENVKGTEDSGTT 193

RESULT 15

US-08-050-319B-2
; Sequence 2, Application US/08050319B
; Patent No. 5633145
; GENERAL INFORMATION:
; APPLICANT: M.Feldmann, P.W. Gray,
; APPLICANT: M.J.C. Turner, F.M. Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,319B
; FILING DATE: 10-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-050-319B-2

Query Match 76.8%; Score 946; DB 1; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.6e-77;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLLPLVLELVGVPSCVIGLVPHLGDREKRDVCPQGYIHPQNNISICT 60
Db 1 MGLSTVPDLLLPLVLELVGVPSCVIGLVPHLGDREKRDVCPQGYIHPQNNISICT 60
QY 61 KCHKGTLYLNDPCPGQDTCRECEGSGFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120
Db 61 KCHKGTLYLNDPCPGQDTCRECEGSGFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120
QY 121 RDTVCGCRKNQRYHYWSENLFQCFNCTCLNGTVHLSCOEKQNTVCT 167
Db 121 RDTVCGCRKNQRYHYWSENLFQCFNCTCLNGTVHLSCOEKQNTVCT 167

Search completed: August 14, 2001, 05:37:07
Job time: 309 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2001, 05:36:18 ; Search time 8.9 Seconds
(without alignments)
842.916 Million cell updates/sec

Title: US-09-599-400A-9

Perfect score: 1231

Sequence: 1 MGLSTVPDLLPLVLELLV.....ENVKGTEDSGTVLLPLVRP 219

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	1219	99.0	455	1	TNR1_HUMAN	P19438	homo sapien
2	906.5	73.6	461	1	TNR1_PIG	P50555	sus scrofa
3	879.5	71.4	454	1	TNR1_MOUSE	P22118	mus musculus
4	867	70.4	461	1	TNR1_RAT	P22934	rattus norv
5	859.5	69.8	471	1	TNR1_BOVIN	O19131	bos taurus
6	216.5	17.6	435	1	TNR1_HUMAN	P36941	homo sapien
7	208	16.9	417	1	WSL1_HUMAN	Q93038	h wsl-1 pro
8	202	16.4	427	1	NGFR_HUMAN	P08138	homo sapien
9	200	16.2	326	1	VT2_MXVL	P29825	myxoma viru
10	189	15.4	325	1	VT2_SFVKA	P25943	shope fibro
11	188	15.3	425	1	NGFR_RAT	P07174	rattus norv
12	186.5	15.2	332	1	FASA_PIG	O77736	sus scrofa
13	181.5	14.7	415	1	TNR2_MOUSE	P50284	mus musculus
14	181	14.7	474	1	TNR2_MOUSE	P25119	mus musculus
15	180.5	14.7	327	1	FASA_MOUSE	P25446	mus musculus
16	174	14.1	289	1	CD40_MOUSE	P27512	mus musculus
17	172	14.0	269	1	CD40_BOVIN	Q28203	bos taurus
18	166.5	13.5	323	1	FASA_BOVIN	P51867	bos taurus
19	164	13.3	349	1	VC22_VARV	P34015	variola vir
20	162.5	13.2	461	1	TNR2_HUMAN	P20333	homo sapien
21	159.5	13.0	416	1	NGFR_CHICK	P18519	gallus gall
22	153.5	12.5	324	1	FASA_RAT	Q63199	rattus norv
23	148	12.0	277	1	CD40_HUMAN	P25942	homo sapien
24	143.5	11.7	1680	1	FUR2_DROME	P30432	drosophila
25	143	11.6	250	1	CD27_MOUSE	P41272	mus musculus
26	140	11.4	687	1	VS41_GIALA	P21227	giardia lam
27	138.5	11.3	260	1	CD27_HUMAN	P26842	homo sapien
28	137.5	11.2	335	1	FASA_HUMAN	P25445	homo sapien
29	137.5	11.2	1877	1	PK5_MOUSE	Q04592	mus musculus
30	135.5	11.0	595	1	CD30_HUMAN	P28908	homo sapien
31	135.5	11.0	1696	1	PK5_BRACL	Q9n115	branchiost
32	135	11.0	272	1	OX40_MOUSE	P47741	mus musculus
33	132	10.7	913	1	PK5_HUMAN	Q92824	homo sapien

ALIGNMENTS

RESULT 1	TNR1_HUMAN	STANDARD;	PRT;	455 AA.
ID	TNR1_HUMAN	STANDARD;	PRT;	455 AA.
AC	P19438;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 1) (TBPI) (P60) (TNF-R1) (TNF-R1) (P55) (CD120A).			
GN	TNFRSF1A OR TNFR1 OR TNFAR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=90235285; PubMed=2158863;			
RA	Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,			
RA	Getanaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.;			
RT	"Molecular cloning and expression of a receptor for human tumor necrosis factor."			
RL	Cell 61:361-370(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90235284; PubMed=2158862;			
RA	Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,			
RA	Tabuchi H., Lesslauer W.;			
RT	"Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor."			
RL	Cell 61:351-359(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.			
RX	MEDLINE=910906021; PubMed=1698610;			
RA	Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zwang R.,			
RA	Aderka D., Hollmann H., Wallach D.;			
RT	"Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type I TNF-R, cloned using amino acid sequence data of its soluble form, encodes both the cell surface and a soluble form of the receptor."			
RL	EMBO J. 9:3269-3278(1990).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91090841; PubMed=1702293;			
RA	Himmeler A., Maurer-Foxy I., Kroenke M., Scheurich P., Pfizenmaier K.,			
RA	Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;			
RT	"Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein."			
RL	DNA Cell Biol. 9:705-715(1990).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	TISSUE=Placenta;			
RC	MEDLINE=91017509; PubMed=2170974;			
RA	Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.;			
RT	"Cloning of human tumor necrosis factor (TNF) receptor cDNA and			

Q21313 caenorhabdi
P15725 rattus norv
P43489 homo sapien
O70433 mus musculu
Q61982 mus musculu
P11046 drosophila
Q00918 rattus norv
Q99088 xenopus lae
O35115 rattus norv
P18751 xenopus lae
Q03185 giardia lam
Q14192 homo sapien

34 130.5 10.6 3672 1 LML2_CAREL
35 126.5 10.3 271 1 OX40_RAT
36 124.5 10.1 277 1 OX40_HUMAN
37 119 9.7 279 1 SLI3_MOUSE
38 119 9.7 2318 1 NTC3_MOUSE
39 118 9.6 1790 1 LMBL_DROME
40 117 9.5 1712 1 TGFB_RAT
41 116.5 9.5 892 1 LDL2_XENLA
42 116 9.4 279 1 SLI3_RAT
43 116 9.4 898 1 ZO71_XENLA
44 115.5 9.4 667 1 TS11_GIALA
45 115 9.3 279 1 SLI3_HUMAN

expression of recombinant soluble TNF-binding protein.";
[6] Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).

RA MEDLINE-92250049; PubMed-131517;
Fuchs P., Strehl S., Dworak M., Himmeler A., Ambros P.F.;
RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
localization to chromosome 12p13.";
RT Genomics 13:219-224(1992).
[7]
RN SEQUENCE OF 41-45.
RX MEDLINE-90110215; PubMed-2153136;
RA Engelmann H., Novick D., Wallach D.;
RT "Two tumor necrosis factor-binding proteins purified from human
urine. Evidence for immunological cross-reactivity with cell surface
tumor necrosis factor receptors.";
RL J. Biol. Chem. 265:1531-1536(1990).
[8]
RN X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.
RX MEDLINE-93258809; PubMed-8387891;
RA Banner D.W., D'Arcy A., Jones W., Gentz R., Schoenfeld H.-J.,
Broger C., Loetscher H., Lesslauer W.;
RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
beta complex: implications for TNF receptor activation.";
RL Cell 73:431-445(1993).
[9]
RN X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
RX MEDLINE-97094982; PubMed-8939750;
RA Naismith J.H., Devine T.Q., Khono H., Sprang S.R.;
RT "Structures of the extracellular domain of the type I tumor necrosis
factor receptor.";
RL Structure 4:1251-1262(1996).

CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
PROTEASES) MEDIATING APOPTOSIS. CONTRIBUTES TO THE INDUCTION OF
NONCYTOTOXIC TNF EFFECTS INCLUDING ANTI-VIRAL STATE AND ACTIVATION
OF THE ACID SPHINGOMYELINASE.

CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
NF-KAPPA B SIGNALING.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO
THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH
NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.

CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -!- SIMILARITY: CONTAINS A DEATH DOMAIN.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD120a entry;
WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120a.htm".

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or send an email to license@isb-sib.ch).

DR EMBL; X55313; CAA39021.1; -
DR EMBL; M33294; AAA03210.1; -
DR EMBL; M58286; AAA36753.1; -
DR EMBL; M63121; AAA36754.1; -
DR EMBL; M75866; AAA61201.1; -
DR EMBL; M75864; AAA61201.1; JOINED.
DR EMBL; M75865; AAA61201.1; JOINED.
DR EMBL; M60275; AAA36756.1; -

DR EMBL; A21522; CAA01558.1; -
DR PIR; A34899; GQHUT1.
DR PIR; A35010; A35010.
DR PIR; S12057; S12057.
DR PIR; A38208; A38208.
DR PDB; 1TNR; 31-JUL-94.
DR PDB; 1NCF; 07-DEC-95.
DR PDB; 1EXT; 11-JAN-97.
DR MIM; 191190; -
DR InterPro; IPR000488; -
DR InterPro; IPR001388; -
DR Pfam; PF00020; TNFR_c6; 4.
DR Pfam; PF00531; death; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00505; TNFR_NGFR_2; 3.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
KW Receptor; transmembrane; Glycoprotein; Repeat; Signal; Apoptosis;
KW 3D-structure.
KW SIGNAL 1 21
FT CHAIN 22 455 TUMOR NECROSIS FACTOR RECEPTOR 1.
FT CHAIN 41 291 TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
FT DOMAIN 22 211 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 212 234 POTENTIAL.
FT DOMAIN 235 455 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 43 196 4 X TNFR-CYS.
FT REPEAT 43 82 TNFR-CYS 1.
FT REPEAT 83 125 TNFR-CYS 2.
FT REPEAT 126 166 TNFR-CYS 3.
FT REPEAT 167 196 TNFR-CYS 4.
FT DOMAIN 338 348 N-SMASE ACTIVATION DOMAIN (NSD).
FT DOMAIN 356 441 DEATH DOMAIN.
FT DISULFID 44 58
FT DISULFID 59 72
FT DISULFID 62 81
FT DISULFID 84 99
FT DISULFID 102 117
FT DISULFID 105 125
FT DISULFID 127 143
FT DISULFID 146 158
FT DISULFID 149 166
FT DISULFID 168 179
FT DISULFID 182 191
FT DISULFID 185 195
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 412 412 MISSING (IN REF. 4).
FT CONFLICT 443 446 GPAA -> APP (IN REF. 4).
SQ SEQUENCE 455 AA; 50494 MW; 4CEPBA96D03B8225 CRC64;

Query Match 99.0%; Score 1219; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 3.le-95;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLLVLELLVGIYPSGVIGVPLHGLDREKRDVCPQGYTHPQNNISCTT 60
DB 1 MGLSTVPDLLLVLELLVGIYPSGVIGVPLHGLDREKRDVCPQGYTHPQNNISCTT 60
QY 61 KCHKGYLYNDVCPGQDTCRCESGFTASENHLRHCLSCSKCKRMQVEISSCTVD 120
DB 61 KCHKGYLYNDVCPGQDTCRCESGFTASENHLRHCLSCSKCKRMQVEISSCTVD 120
QY 121 RDTVCCKRKNQRYHWSNENLFCQFNCSLCLNGTVHLSQCKQNTVCTCHAGFFLRENECV 180
DB 121 RDTVCCKRKNQRYHWSNENLFCQFNCSLCLNGTVHLSQCKQNTVCTCHAGFFLRENECV 180
QY 181 SCNCKKSLCTKLCPLQIENVGKTEDSGTTLPLV 217
DB 181 SCNCKKSLCTKLCPLQIENVGKTEDSGTTLPLV 217

RESULT 2

TNRL_PIG STANDARD; PRT; 461 AA.

AC P50555;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (TNF-R1) (P55).

GN TNFRSF1A OR TNFR1.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RX MEDLINE=96011645; PubMed=7590278;

RA Suter B., Pauli U.H.;

RT "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.";

RL Gene 163:263-266(1995).

CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).

CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

CC -----

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CC -----

DR EMBL; U19994; AAC48499.1; -.

DR HSP; P19438; 1TNR.

DR InterPro; IPR000488; -.

DR InterPro; IPR001368; -.

DR Pfam; PF00020; TNFR_c6; 3.

DR Pfam; PF00531; death; 1.

DR PROSITE; PS00652; TNFR_NGFR_1; 3.

DR PROSITE; PS50050; TNFR_NGFR_2; 2.

DR PROSITE; PS50017; DEATH_DOMAIN; 1.

KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.

FT SIGNAL 1 21

FT CHAIN 22 461

FT DOMAIN 22 210

FT TRANSMEM 211 233

FT DOMAIN 234 461

FT DOMAIN 43 195

FT REPEAT 43 82

FT REPEAT 83 125

FT REPEAT 126 166

FT REPEAT 167 195

FT DOMAIN 340 350

FT DOMAIN 362 447

FT DISULFID 44 58

FT DISULFID 59 72

FT DISULFID 62 81

FT DISULFID 84 99

FT DISULFID 102 117 BY SIMILARITY.

FT DISULFID 105 125 BY SIMILARITY.

FT DISULFID 127 143 BY SIMILARITY.

FT DISULFID 146 158 BY SIMILARITY.

FT DISULFID 149 166 BY SIMILARITY.

FT DISULFID 168 179 BY SIMILARITY.

FT DISULFID 182 190 BY SIMILARITY.

FT DISULFID 185 194 BY SIMILARITY.

FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 151 151 N-LINKED (GLCNAC. .) (POTENTIAL).

SQ SEQUENCE 461 AA; 50696 MW; CD72361EC60C9D43 CRC64;

Query Match 73.6%; Score 906.5; DB 1; Length 461;

Best Local Similarity 74.7%; Pred. No. 4.7e-69;

Matches 162; Conservative 16; Mismatches 38; Indels 1; Gaps 1;

QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDRKRSVCPQGYIHPQNNISICT 60

Db 1 MGLSTVPGLLLPLVLRALLVDVYAGVHGLVHPGDREKRESLCPQGYKSHYPQNRISICT 60

QY 61 KCHKGTLYNDPCPGQDTCRECESSGFTASENHLRHLCSCKRCKEMGQVEISSCTVD 120

Db 61 KCHKGTLYLHNDCLGPDTCRECDNGTFTASENHLTQCLSCSKRSEMSQVEISPTVD 120

QY 121 RDTVCGGRKNQRYHWSENLFCQFCNCSLNGTVHLSQEKQNTVCTCHAGFFLRENECV 180

Db 121 RDTVCGGRKNQRYHWSENLFCQFCNCSLNGTVHLSQEKQNTVCTCHAGFFLRENECV 180

QY 181 SCSCNCKSLECTKCLPQIENVKGTEDSGTVLLPLV 217

Db 181 SCVCKNA-DCKNLCPATSETRDNFDQDTGTVLLPLV 216

RESULT 3

TNRL_MOUSE STANDARD; PRT; 454 AA.

AC P25118;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (TNF-R1) (P55).

GN TNFRSF1A OR TNFR1 OR TNFR-1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91187885; PubMed=1849278;

RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H., Chen E.Y., Goeddel D.V.;

RT "Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.";

RT Spec. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=91246168; PubMed=1645445;

RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A.;

RT "Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor.";

RL Mol. Cell. Biol. 11:3020-3026(1991).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=91285014; PubMed=1647956;

RX Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissonerghis A.M., Gray P.W., Feldmann M., Foxwell B.M.J.;

RT "Cloning, expression and cross-linking analysis of the murine p55


```

FT CHAIN 22 471 TUMOR NECROSIS FACTOR RECEPTOR 1.
FT DOMAIN 22 210 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 211 233 POTENTIAL.
FT DOMAIN 234 471 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 43 195 4 X TNFR-CYS.
FT REPEAT 43 82 TNFR-CYS 1.
FT REPEAT 83 125 TNFR-CYS 2.
FT REPEAT 126 166 TNFR-CYS 3.
FT REPEAT 167 195 TNFR-CYS 4.
FT DOMAIN 340 360 N-SMASE ACTIVATION DOMAIN (NSD).
FT DOMAIN 372 457 DEATH DOMAIN.
FT DISULFID 44 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 82 81 BY SIMILARITY.
FT DISULFID 84 99 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 143 BY SIMILARITY.
FT DISULFID 146 158 BY SIMILARITY.
FT DISULFID 149 166 BY SIMILARITY.
FT DISULFID 168 179 BY SIMILARITY.
FT DISULFID 182 190 BY SIMILARITY.
FT DISULFID 185 194 BY SIMILARITY.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 471 AA: 51367 MW; 5243EF514DFE81C4 CRC64;

Query Match 69.8%; Score 859.5; DB 1; Length 471;
Best Local Similarity 69.6%; Pred. No. 4.1e-65;
Matches 151; Conservative 22; Mismatches 43; Indels 1; Gaps 1;

QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDRKDSVCPQGYIHPONNSICT 60
DB 1 MGLTVPGLLLPLVLPALLADVPAGVGLVPHGDLKRESQPGKYNHPONSTICT 60

QY 61 KCHKGTLYNDPCPGQDPTDCRECSGSFTASENHLRHLCSCKRKGQVSISSCTVD 120
DB 61 KCHKGTLYNDPCPGQDPTDCRCVAGTGTALENHLRCLSCRCRDEMFOVSISSCTVD 120

QY 121 RDTVCGCRNQYRHYWSENLFQCFNCSLCLNGTGVHLSQEQKNTVCTCHAGFFLRENECV 180
DB 121 RDTVCGCRNQYRHYWSENLFQCFNCSLCLNGTGVHLSQEQKNTVCTCHAGFFLRENECV 180

QY 181 SCSNCKSKSECTKLCPLQIENVKGTEDSGTIVLLPLV 217
DB 181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTIVLLPLV 216

RESULT 6
TNRC_HUMAN STANDARD; PRT: 435 AA.
AC P36941;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
DE 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
GN LTBR OR TNFR OR TNFRSF3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93252381; PubMed=8486360;
RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT "Construction and evaluation of a hncDNA library of human l2p
RT transcribed sequences derived from a somatic cell hybrid.";
RL Genomics 16:214-218(1993).
RN [2]

```

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RP FUNCTION.
RX MEDLINE=94225209; PubMed=8171323;
RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT "A lymphotoxin-beta-specific receptor.";
RL Science 264:707-710(1994).
CC -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC -----
CC EMBL; L04270; AAA36757.1; -.
CC HSSP; P25942; 1CDF.
CC MIM; 600979; -.
CC InterPro; IPR001368; -.
CC Pfam; PF00020; TNFR_C6; 4.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS50050; TNFR_NGFR_2; 3.
CC Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 435 LYMPHOTOXIN-BETA RECEPTOR.
FT DOMAIN 31 227 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 228 248 POTENTIAL.
FT DOMAIN 249 435 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 211 4 X TNFR-CYS.
FT REPEAT 42 81 TNFR-CYS 1.
FT REPEAT 82 124 TNFR-CYS 2.
FT REPEAT 125 168 TNFR-CYS 3.
FT REPEAT 169 211 TNFR-CYS 4.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 80 BY SIMILARITY.
FT DISULFID 83 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
FT DISULFID 104 124 BY SIMILARITY.
FT DISULFID 126 132 BY SIMILARITY.
FT DISULFID 139 148 BY SIMILARITY.
FT DISULFID 142 167 BY SIMILARITY.
FT DISULFID 170 185 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 435 AA; 46709 MW; 624626E6022F656F CRC64;

Query Match 17.6%; Score 216.5; DB 1; Length 435;
Best Local Similarity 32.0%; Pred. No. 2.7e-11;
Matches 71; Conservative 23; Mismatches 103; Indels 25; Gaps 12;

QY 2 GLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDRK-RDSVCPQGYIHPONNSICT 60
DB 11 GLWGP---LVGLGLAASQPAQ---PPYASENQTCDQ---EKEYEPQHR-ICCS 60

QY 61 KCHKGTLYNDPCPGQDPTDCRECSGSFTASENHLRHLCSCKRKGQVSISSCTVD 120
DB 61 RCPPTVVSAC-SRIEDTVCAENSYNEHWNLYITCQLCRPCDPVMGLEEAPCTSK 119

QY 121 RDTVCGCRNQYRHYWSENLFQCFNCSL---CLNGTVHLSQEQ--KONTVCT-CHAGFFL 174
DB 120 RKTQCRQCPGMFCAAWA---LECTHCELLSDCPPTGAELKDEVGKGNHVCPCAGHF- 175

QY 175 RENEVCSNCKSKSECTKLCPLQIENVKGTEDSGTIVLLPL 216
DB 176 -QNTSPSARCQPHTRCENQGL--VEAAPTQASDITCKNPL 214

```

RESULT 7
WSL1_HUMAN STANDARD; PRT; 417 AA.
AC Q93038; Q93036; Q93037; Q92983; P78515; Q99831; Q99722; P78507;
AC Q99830;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE WSL-1 PROTEIN PRECURSOR (APOPTOSIS-MEDIATING RECEPTOR DR3) (APOPTOSIS-
DE MEDIATING RECEPTOR TRAMP) (DEATH DOMAIN RECEPTOR 3) (WSL PROTEIN)
DE (APOPTOSIS INDUCING RECEPTOR AIR) (APO-3) (LYMPHOCYTE ASSOCIATED
DE RECEPTOR OF DEATH) (LARD).
GN TNFRSF12 OR WSL1 OR WSL OR APO3 OR DR3 OR DR3.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND MUTAGENESIS.
RC TISSUE=Lymphoid;
RX MEDLINE=97088617; PubMed=8934525;
RA Kitson J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T.,
RA Grinham C.J., Brown R., Farrow S.N.; that mediates apoptosis.";
RT "A death-domain-containing receptor that mediates apoptosis.";
RL Nature 384:372-375(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Umbilical vein endothelial cells;
RX MEDLINE=97081063; PubMed=8875942;
RA Chinnaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M.,
RA Duan D.R., Xing L., Gentz R., Ni J., Dixit V.M.;
RT "Signal transduction by DR3, a death domain-containing receptor
RT related to TNFR-1 and CD95.";
RL Science 274:990-992(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=97148200; PubMed=8994832;
RA Marsters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L.,
RA Goddard A.D., Bauer K.D., Ashkenazi A.;
RT "Apo-3, a new member of the tumor necrosis factor receptor family,
RT contains a death domain and activates apoptosis and NF-kappa-B.";
RL Curr. Biol. 6:1669-1676(1996).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=9727273; PubMed=9114039;
RA Screaton G.R., Xu X.-N., Olsen A.L., Cowper A.E., Tan R.,
RA McMichael A.J., Bell J.I.;
RT "LARD: a new lymphoid-specific death domain containing receptor
RT regulated by alternative pre-mRNA splicing.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
RN [6]
RP SEQUENCE OF 4-417 FROM N.A.
RC TISSUE=Brain, and Fetal lung;
RX MEDLINE=97205335; PubMed=9052839;
RA Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,
RA Thome M., Bornand T., Hahne M., Schroeter M., Wilson A., French L.E.,
RA Browning J.B., Macdonald H.R., Tschopp J.;
RT "TRAMP, a novel apoptosis-mediating receptor with sequence homology
RT to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95).";
RL Immunity 6:79-88(1997).
RN [7]
RP SEQUENCE OF 7-417 FROM N.A.
RC TISSUE=Brain;
RX Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RA Chaudhary P.M., Hood L.E.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INDUCES APOPTOSIS AND ACTIVATES NUCLEAR FACTOR KAPPA-B
CC (NF-KAPPAB). DIRECTLY INTERACTS WITH TRADD ADAPTOR MOLECULE. MAY
CC PLAY A ROLE IN REGULATING LYMPHOCYTE HOMEOSTASIS.

CC -1- SUBUNIT: HOMODIMER. INTERACTS STRONGLY VIA THE DEATH DOMAINS WITH
CC THE TNFR1-ASSOCIATED MOLECULE TRADD AND THE TNFR1 RECEPTOR TO
CC ACTIVATE AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC NF-KAPPA B SIGNALING.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; WSL-1/LARD-1A (SHOWN HERE),
CC WSL-SI/LARD-3 AND WSL-S2; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND
CC LYMPHOCYTES. DETECTED IN LYMPHOCYTE-RICH TISSUES SUCH AS THYMUS,
CC COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.
CC -1- PTM: GLYCOSYLATED (PROBABLE).
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y09392; CAA70561.1; -
CC EMBL; Y09392; CAA70559.1; -
CC EMBL; Y09392; CAA70560.1; -
CC EMBL; U72763; AAC50819.1; -
CC EMBL; U83599; AAB41434.1; -
CC EMBL; U83600; AAB41435.1; -
CC EMBL; U78029; AAB40918.1; -
CC EMBL; U74611; AAB39714.1; -
CC EMBL; U94501; AAC51306.1; -
CC EMBL; U94504; AAC51309.1; -
CC EMBL; U75380; AAC51192.1; -
CC EMBL; U75381; AAC51193.1; -
CC HSSP; P19438; AAB41432.1; -
CC MIM; 603366; -
CC InterPro: IPR000488; -
CC InterPro: IPR001368; -
CC Pfam; PF00020; TNFR_c6; 2.
CC Pfam; PF00531; death; 1.
CC PROSITE; PS00652; TNFR_NGFR1; 2.
CC PROSITE; PS00050; TNFR_NGFR2; 1.
CC PROSITE; PS00017; DEATH_DOMAIN; 1.
CC Receptor; Apoptosis; Alternative splicing; Transmembrane; Signal;
KW Repeat.
KW SIGNAL 1 24
FT CHAIN 25 417
FT DOMAIN 25 199
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 200 220
FT POTENTIAL.
FT DOMAIN 223 417
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 34 192
FT REPEAT 34 71
FT REPEAT 72 115
FT REPEAT 116 163
FT REPEAT 164 192
FT REPEAT 332 413
FT DEATH DOMAIN.
FT DOMAIN 332 413
FT CARBOHYD 67 67
FT CARBOHYD 106 106
FT VARSPLIC 182 218
FT
FT VARSPLIC 219 417
FT VARSPLIC 200 253
FT
FT
FT
FT
FT VARSPLIC 254 417
FT MUTAGEN 354 354
FT
FT MUTAGEN 356 356
FT
FT MUTAGEN 373 373

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FT FT CONFLICT 4 6 TNFR1 INTERACTION.
FT CONFLICT 60 60 RPR -> AAA (IN REF. 6).
FT CONFLICT 167 167 P -> L (IN REF. 7).
FT CONFLICT 312 312 A -> R (IN REF. 6 AND 7).
FT CONFLICT 370 370 R -> L (IN REF. 1).
FT CONFLICT 381 381 R -> H (IN REF. 1).
FT CONFLICT 381 381 R -> L (IN REF. 1).
SQ SEQUENCE 417 AA; 45385 MW; 5226319DFDB46706 CRC64;

Query Match 16.9%; Score 208; DB 1; Length 417;
Best Local Similarity 28.9%; Pred. No. 1.3e-10;
Matches 57; Conservative 22; Mismatches 86; Indels 32; Gaps 9;

QY 15 LLELLVGIYPSGVIGLVPHLGDREKDSVCPQGYIHPQNNISCTCTKCHKGTLYNDPCG 74
D 15 LLLVLLGARAQG-----GTRSPR---CDCAGDFHKKIGLFCRCGPAGHYLKAPCTE 63
QY 75 PGQDTCRECEGSGFTASENHLR-HCLSCSKRKEMQGVSEISCTVDRDVTVCGRKNQYR 133
D 64 PCGNSTCLVCPQDPTFLAWENHNSCARCOACDEQASQVALENCASAVADTRCGCKFGWF 123
QY 134 HYWSENLFQC-----FNCISCLN-GRVH-----LSCQEKQNTVCTCHAGFFLRENECVSC- 182
D 124 EC---QVSOCVSSPPYCPQCLDCGALHRRLLCSRRDTCGTCLPGFYEHGDCGVSCP 180
QY 183 ----SNCKSLECKLKC 195
D 181 TSTLGSCPE--RCAAVC 195

RESULT 8
NGFR_HUMAN STANDARD; PRT; 427 AA.
AC P08138.
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
DE (GP80-LNGFR). (P75 ICD).
GN NGFR OR TNFRSF16.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87051725; PubMed=3022937;
RA Johnson D., Lanahan A., Buck C.R., Sehgal A., Morgan C., Mercer E.,
RA Bothwell M., Chao M.;
RT "Expression and structure of the human NGF receptor.";
RL Cell 47:545-554(1986).
RN [2]
RP SEQUENCE OF 1-22 FROM N.A.
RX MEDLINE=89095903; PubMed=2850481;
RA Sehgal A., Patil N., Chao M.;
RT "A constitutive promoter directs expression of the nerve growth factor receptor gene.";
RL Mol. Cell. Biol. 8:3160-3167(1988).
CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
CC NT-3, AND NT-4.
CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
CC BOND FORMATION.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC
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CC
CC EMBL; M14764; AAB59544.1; -.
CC EMBL; M21621; AAA36363.1; -.
DR PIR; A25218; GOHUN.
DR HSSP; P07174; INGR.
DR MIM; 162010; -.
DR InterPro; IPR000488; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_c6; 4.
DR Pfam; PF00531; death_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 4.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
KW Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
KW phosphorylation; Signal.
FT SIGNAL 1 28 LOW-AFFINITY NERVE GROWTH FACTOR
FT CHAIN 29 427 RECEPTOR.
FT DOMAIN 29 250 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 251 272 POTENTIAL.
FT DOMAIN 273 427 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 31 189 4 X TNFR-CYS.
FT REPEAT 31 65 TNFR-CYS 1.
FT REPEAT 66 107 TNFR-CYS 2.
FT REPEAT 108 147 TNFR-CYS 3.
FT REPEAT 148 189 TNFR-CYS 4.
FT DOMAIN 344 421 DEATH DOMAIN.
FT DISULFID 32 43 BY SIMILARITY.
FT DISULFID 44 57 BY SIMILARITY.
FT DISULFID 47 64 BY SIMILARITY.
FT DISULFID 67 83 BY SIMILARITY.
FT DISULFID 86 99 BY SIMILARITY.
FT DISULFID 89 107 BY SIMILARITY.
FT DISULFID 109 122 BY SIMILARITY.
FT DISULFID 125 138 BY SIMILARITY.
FT DISULFID 128 146 BY SIMILARITY.
FT DISULFID 149 164 BY SIMILARITY.
FT DISULFID 167 180 BY SIMILARITY.
FT DISULFID 170 188 BY SIMILARITY.
FT DOMAIN 197 248 SER/THR-RICH.
FT CARBOHYD 60 60 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 427 AA; 45183 MW; B09FA143FB3D625B CRC64;

Query Match 16.4%; Score 202; DB 1; Length 427;
Best Local Similarity 29.8%; Pred. No. 4.4e-10;
Matches 61; Conservative 30; Mismatches 78; Indels 36; Gaps 12;

QY 12 PLVLELLVGIYPSGVIGLVPHLGDREKDSVCPQGYIHPQNNISCTCTKCHKGTLYND 71
D 13 PRLLLLLLGVSLGA-----KEACTPTGLYTH---SGECKACNLGEGVAQP 56
QY 72 CPGPGQDTCREC-ESGFTASENHLRHLCSCKRKEMQGVSEISS-CTVDRDVTVCGRK 129
D 57 C-GANQ-TVCEPCLDSYTFSDVVSATPECPKPTCEC---VGLQSMASAPCVADDVAVCR-- 109
QY 130 NQYHYWSENLFQCNCISCLNGT-VHLSQOEKQNTVC-TCHAGFFLRE----NECVSCS 183
D 110 -AYGYQDETTRGCRACRVCAGSLVFCQDKQNTVCEECPDGTYSDEANHVDPCLPT 168
QY 184 NC-----KKSLECKLCLPQIENVKG 204
D 169 VCEDTQRQLRECTRWADAECIEIFG 193

RESULT 9
VT2_MXVL
ID VT2_MXVL STANDARD; PRT; 326 AA.
AC P29825;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
```

DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN T2.
OS Myxoma virus (strain Lausanne).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
OX NCBI_TaxID=31530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91335768; PubMed=1651597;
RA Upton C., Macen J.L., Schreiber M., McFadden G.;
RT "Myxoma virus expresses a secreted protein with homology to the tumor
RT necrosis factor receptor gene family that contributes to viral
RT virulence.";
RL Virology 184:370-382(1991).
CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
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CC
CC EMBL; M95181; AAA46632.1; -;
CC EMBL; A23729; CAA01688.1; -;
CC PIR; A40566; GQVZML.
CC HSSP; P19438; 1TNR.
CC InterPro: IPR001368; -;
CC Pfam: PF00020; TNFR_C6; 2.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS50050; TNFR_NGFR_2; 2.
CC Receptor; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 16
FT CHAIN 17 326 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
FT DOMAIN 27 186 4 X TNFR-CYS.
FT REPEAT 27 62 TNFR-CYS 1.
FT REPEAT 63 104 TNFR-CYS 2.
FT REPEAT 105 147 TNFR-CYS 3.
FT REPEAT 148 186 TNFR-CYS 4.
FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 326 AA; 35208 MW; ABBF027E947292FF CRC64;

Query Match 16.2%; Score 200; DB 1; Length 326;
Best Local Similarity 25.8%; Pred. No. 5.1e-10;
Matches 62; Conservative 28; Mismatches 88; Indels 62; Gaps 10;

QY 14 VLELLGVIPSGVIGLVPHLGDREKRDSCVCPQGYKIHPPQNNSTCCCKHKGTYLNDGP 73
DB 6 LLLAYACVYGGG----APYGADRGK----CRGNDY---EKDGLCCSCPPGYSASRLC- 53
QY 74 GPQDQDCRECESGSFTASENHLRHCLSC-SKCRKEMGOVEISSCTVDRTVCGRKNOY 132
DB 54 GPQSDTVCSCKNETFTFASTNHAPACVSCRGCRGTGHLIS--ESQSCDTRDRVDCSAGNY 111
QY 133 -----RHYSENLFQCFNCSLCLNG- 152
DB 112 CLLKGQGCRCAPKTKCPAGYGVSHRTGDLVLTCKPRTYTSYDAVSSFTCTSSFYI 171
QY 153 TVHLSQOEKQNTVCTCHAGFFLRENECVSCNCKSL---ECTKLCLPQIENVRKGTDSG 209
DB 172 SVEFNLYPVNDTCTTTAG----PNEVVKTSEFVTLNHTDCDPVFHTYYGTSSSEGAG 227

RESULT 10

VT2_SFVKA
ID VT2_SFVKA STANDARD; PRT; 325 AA.
AC P25943;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN T2.
OS Shope fibroma virus (strain Kasza) (SFV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
OX NCBI_TaxID=10272;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87321103; PubMed=2820128;
RA Upton C., Delange A.M., McFadden G.;
RT "Tumorigenic poxviruses: genomic organization and DNA sequence of the
RT telomeric region of the Shope fibroma virus genome.";
RL Virology 160:20-30(1987).
RN [2]
RN FUNCTION.
RP MEDLINE=91207415; PubMed=1850261;
RX Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,
RA McFadden G., Goodwin R.G.;
RT "T2 open reading frame from the Shope fibroma virus encodes a soluble
RT form of the TNF receptor.";
RL Biochem. Biophys. Res. Commun. 176:335-342(1991).
CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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CC
CC EMBL; M17433; -; NOT_ANNOTATED_CDS.
CC EMBL; A23727; CAA01687.1; -;
CC PIR; B43692; B43692.
CC HSSP; P19438; 1TNR.
CC InterPro: IPR001368; -;
CC Pfam: PF00020; TNFR_C6; 2.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS50050; TNFR_NGFR_2; 1.
CC Receptor; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 16
FT CHAIN 17 325 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
FT DOMAIN 27 186 4 X TNFR-CYS.
FT REPEAT 27 62 TNFR-CYS 1.
FT REPEAT 63 104 TNFR-CYS 2.
FT REPEAT 105 147 TNFR-CYS 3.
FT REPEAT 148 186 TNFR-CYS 4.
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 325 AA; 35132 MW; 810530339198A71E CRC64;

Query Match 15.4%; Score 189; DB 1; Length 325;
Best Local Similarity 27.7%; Pred. No. 4.2e-09;
Matches 57; Conservative 25; Mismatches 82; Indels 42; Gaps 10;

QY 9 LLLPLVLELLGVIPSGVIGLVPHLGDREKRDSCVCPQGYKIHPPQNNSTCCCKHKGTYL 68
DB 1 MLRLIALLVCVYVYGGD---VPYSSNQK---CGGHDY---EKDGLCCACHPGFYA 49
QY 69 YNDPCPGQDQDCRECESGSFTASENHLRHCLSC-SKCRKEMGOVEISSCTVDRTVCGR 127

Db 50 SRLC-GPGSNTVCSPECDGTFTASTNHAPACVSCRCPCGTGHLIS--ESQPCDRTHDRVCNC 106
 QY 128 RKNQYRHYWSENLFQCNGLNCTVHLSCQEKQNTVCTCHAGFFLRNECVSCSNCKK 187
 Db 107 STGNYCLLKQGN-----GCRICAPQT-----KCPAGYGVSGHTRAGDTLCEK 148
 QY 198 SLECKTLCLPQI--ENVKTEDSGTT 211
 Db 149 -----CPPHYTSLSLSPTRCGTS 167
 RESULT 11
 NGFR_RAT STANDARD; PRT:- 425 AA.
 AC P07174;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
 DE (GP80-LNGFR) (P75 ICD).
 GN NGFR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID-10116;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87115859; PubMed-3027580;
 RA Radeke M.J., Misko T.P., Hsu C., Herzenberg L.A., Shooter E.M.;
 RT "Gene transfer and molecular cloning of the rat nerve growth factor
 receptor.";
 RL Nature 325:593-597(1987).
 [2]
 RN SEQUENCE OF 1-22 FROM N.A.
 RP TISSUE=Liver;
 RC MEDLINE-93077038; PubMed-1446821;
 RA Metsis M., Timusk T., Allikmets R., Saarma M., Persson H.;
 RT "Regulatory elements and transcriptional regulation by testosterone
 and retinoic acid of the rat nerve growth factor receptor promoter.";
 RL Gene 121:247-254(1992).
 [3]
 RN STRUCTURE BY NMR OF 334-418.
 RX MEDLINE-97449145; PubMed-9305641;
 RA Lipezhn E., Ilag L.L., Otting G., Ibanez C.F.;
 RT "NMR structure of the death domain of the p75 neurotrophin receptor.";
 RL EMBO J. 16:4999-5005(1997).
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
 CC NT-3, AND NT-4.
 CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
 CC BOND FORMATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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 DR EMBL; X05137; CAA28783.1; -
 DR EMBL; X61269; -; NOT_ANNOTATED_CDS.
 DR PIR; A26431; A26431.
 DR PDB; INGR; 29-JUL-97.
 DR InterPro; IPR000488; -
 DR InterPro; IPR001368; -
 DR Pfam; PF00020; TNFR_c6; 4.
 DR Pfam; PF00531; death; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PROSITE; PS50050; TNFR_NGFR_2; 4.

DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 KW Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
 FT SIGNAL 1 29
 FT CHAIN 30 425 LOW-AFFINITY NERVE GROWTH FACTOR
 FT RECEPTOR.
 FT DOMAIN 30 251 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 252 273 POTENTIAL.
 FT DOMAIN 274 425 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 32 190 4 X TNFR-CYS.
 FT REPEAT 32 66 TNFR-CYS 1.
 FT REPEAT 67 108 TNFR-CYS 2.
 FT REPEAT 109 148 TNFR-CYS 3.
 FT REPEAT 149 190 TNFR-CYS 4.
 FT DOMAIN 198 249 SER/THR-RICH.
 FT DOMAIN 354 419 DEATH DOMAIN.
 FT DISULFID 33 44 BY SIMILARITY.
 FT DISULFID 45 58 BY SIMILARITY.
 FT DISULFID 48 65 BY SIMILARITY.
 FT DISULFID 68 84 BY SIMILARITY.
 FT DISULFID 87 100 BY SIMILARITY.
 FT DISULFID 90 108 BY SIMILARITY.
 FT DISULFID 110 123 BY SIMILARITY.
 FT DISULFID 126 139 BY SIMILARITY.
 FT DISULFID 129 147 BY SIMILARITY.
 FT DISULFID 150 165 BY SIMILARITY.
 FT DISULFID 168 181 BY SIMILARITY.
 FT DISULFID 171 189 BY SIMILARITY.
 FT CARBOHYD 61 61 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 71 71 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 425 AA; 45432 MW; B2E152D94D3827F8 CRC64;
 Query Match 15.3%; Score 188; DB 1; Length 425;
 Best Local Similarity 28.6%; Pred. No. 6.4e-09;
 Matches 58; Conservative 30; Mismatches 79; Indels 36; Gaps 12;
 QY 14 VLELLVGIYPSGVIGLVPHLGDREKRDSVCPQSGKYIHPQNNISCTCKHKGTLYNDGP 73
 Db 16 LLLLLILGVSSGGA-----KETCSTGLYTH---SGECCKACNLGEGVAQPC- 58
 QY 74 GPGQDTCREC-ESGSFTASENHLRCLSCSKCKEMQVEISS-CHVDRTVCGCRKNQ 131
 Db 59 GANQ-TVCEPCLDNTVFSVDATEPCPKPCTEC---LGLQSMSPACVADDAVCRC---A 111
 QY 132 YRYWSENLPQCNCISCLNGT-VHLSCQEKQNTVC-TCHAGFFLR-----NECVSCSN 185
 Db 112 YGYQEETHCHCEACSVCEVSGLVFSCQDKQNTVCECEPGIYSDEANHVDPCLDCTVC 171
 QY 186 ----KKSLECTKLCLPQIENVKG 204
 Db 172 EDTERQLRECTPWADAECEIIPG 194
 RESULT 12
 FASA_PIG STANDARD; PRT; 332 AA.
 ID FASA_PIG
 AC 07736;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
 DE (APO-1 ANTIGEN) (CD95).
 GN TNFRSF6 OR APT1 OR FAS.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID-9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darner D.;
 RT "Expression of apoptosis-associated genes in hibernating and stunned
 myocardium of pig.";

RN [2]
RP SEQUENCE OF 1-96 FROM N.A.
RX MEDLINE=93189576; PubMed=7680478;
RA Adachi M., Watanabe-Fukunaga R., Nagata S.;
RT "Aberrant transcription caused by the insertion of an early
transposable element in an intron of the Fas antigen gene of lpr
mice.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:1756-1760(1993).
RN [3]
RP VARIANT LPR.
RX MEDLINE=92195401; PubMed=1372394;
RA Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA Nagata S.;
RT "Lymphoproliferation disorder in mice explained by defects in Fas
antigen that mediates apoptosis.";
RL Nature 356:314-317(1992).
CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS,
LIVER, LUNG, HEART, AND ADULT OVARY.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -!- DISEASE: DEFECTS IN FAS ARE THE CAUSE OF A LYMPHOPROLIFERATION
DISORDER (LPR) RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY
PRODUCTION.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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or send an email to license@isb-sib.ch).

DR EMBL; M83649; AAA37593.1; -;
DR EMBL; S56490; AAB25700.1; -;
DR EMBL; S56485; AAB25700.1; JOINED.
DR EMBL; S56486; AAB25700.1; JOINED.
DR PIR; A46484; A46484.
DR HSP; P25445; 1DDF.
DR MGD; MGI:95484; Fas.
DR InterPro; IPR000488; -;
DR InterPro; IPR001368; -;
DR Pfam; PF00020; TNFR_G6; 3.
DR Pfam; PF00531; death; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal;
KW Disease mutation.
FT SIGNAL 1 21
FT CHAIN 22 327 FASL RECEPTOR.
FT DOMAIN 22 169 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 170 186 POTENTIAL.
FT DOMAIN 187 327 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 43 162 3 X TNFR-CYS.
FT REPEAT 43 79 TNFR-CYS 1.
FT REPEAT 80 123 TNFR-CYS 2.
FT REPEAT 124 162 TNFR-CYS 3.
FT REPEAT 222 306 DEATH DOMAIN.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 246 246 I -> N (IN LPR).

SQ SEQUENCE 327 AA; 37418 MW; F6BFFC5ACE356EEE CRC64;
Query Match 14.7%; Score 180.5; DB 1; Length 327;
Best Local Similarity 25.9%; Pred. No. 2.2e-08;
Matches 55; Conservative 24; Mismatches 94; Indels 39; Gaps 7;
QY 10 LLPVLLELLVGIYPSGVIGLVPHLGDEK---RDSVCPQGYIHPQNNISICTYKCHGT 66
Db 7 VLPVLVLAGSQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLY---QGGPFCCQCPQFK 63
QY 67 YLYNDPCPGQDTCRECESGSFTASENHLR-HCLSCSKCKRMQVEISSCTVDRTVC 125
Db 64 KVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKRCRCRLCDDEEHGLEVETNCTLTQNTKC 123
QY 126 GCRKNQVRHYWSENLFQCFNCSLCLNGTVHLSQCEKQNTVCTCHAGFFELRENECVCSNC 185
Db 124 KCKPDFYCD--SPCEHCVRCAECHEGTLE-PCATATSN-----NC 161
QY 186 KKSLECTKLCPLQIENVKGTEDSGTTVLLPLV 217
Db 162 RKQSPRNLWLLTI-----LVLLIPLV 183
Search completed: August 14, 2001, 05:38:27
Job time: 129 sec

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Sequence
Comparison

RESULT 1
CQUT1
tumor necrosis factor receptor 1 precursor [validated] - human
N:Alternate names: P55 tumor necrosis factor receptor; TNF receptor type 1
N:Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding prot
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 08-Dec-2000
C:Accession: A38208; A34899; A34900; A36555; C36555; A38281; S12057; J07058; A60231;
R:Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
Genomics 13, 219-224, 1992
A:Title: Structure of the human TNF receptor 1 (p60) gene (TNFRF1) and localization to
A:Reference number: A38208; MUID:92250049
A:Accession: A38208
A:Molecule type: DNA
A:Residues: 1-455 <FUC>
A:Cross-references: GB:M75864; GB:M75865; GB:M75866; NID:g339748; PIDN:AAA61201.1; PI
R:Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Less
Cell 61, 351-359, 1990
A:Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor re
A:Reference number: A34899; MUID:90235284
A:Accession: A34899
A:Molecule type: mRNA
A:Residues: 1-455 <LOE>
A:Cross-references: GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36753.1; PID:g339754
A:Experimental source: Placenta
A:Note: part of this sequence, including the amino end of the mature protein, confirm
R:Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga,
Cell 61, 361-370, 1990
A:Title: Molecular cloning and expression of a receptor for human tumor necrosis fact
A:Reference number: A34900; MUID:90235285
A:Accession: A34900
A:Molecule type: mRNA
A:Residues: 1-455 <SCH>
A:Cross-references: GB:M33294; NID:g339744; PIDN:AAA03210.1; PID:g339745
R:Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M
DNA Cell Biol. 9, 705-715, 1990
A:Title: Molecular cloning and expression of human and rat tumor necrosis factor rece
A:Reference number: A36555; MUID:91090841
A:Accession: A36555
A:Molecule type: mRNA
A:Residues: 1-455 <HIM>
A:Cross-references: GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756
A:Accession: C36555
A:Molecule type: protein
A:Residues: 30-38;41-53,'X',55-79,'XX',82-94,'NK','XX',100-104;107-128;162-167,'X',16
R:Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
A:Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of
A:Reference number: A38281; MUID:91017509
A:Accession: A38281
A:Molecule type: mRNA

A:Residues: 1-455 <GRA>
A:Cross-references: GB:M37764
A:Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372
R:Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann
EMBO J. 9, 3269-3278, 1990
A:Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type
le form of the receptor.
A:Reference number: S12057; MUID:91006021
A:Accession: S12057
A:Molecule type: mRNA
A:Residues: 1-455 <NOP>
A:Cross-references: EMBL:X55133; NID:q37223; PIDN:CAA39021.1; PID:q37224
A:Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w
R:Kemper, O.; Wallach, D.
Gene 134, 209-216, 1993
A:Title: Cloning and partial characterization of the promoter for the human p55 tumor ne
A:Reference number: JT0758; MUID:94085779
A:Accession: JT0758
A:Molecule type: DNA
A:Residues: 1-13 <KEM>
R:Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
Eur. J. Immunol. 20, 1167-1174, 1990
A:Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc
A:Reference number: A60231; MUID:90292116
A:Accession: A60231
A:Molecule type: protein
A:Residues: 41-43, 'X', 45-53, 'X', 55-57 <SEC>
R:Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Le
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A:Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto
tients.
A:Reference number: A38258; MUID:91062364
A:Accession: A38258
A:Molecule type: protein
A:Residues: 41-60 <GAR>
A:Experimental source: cancer patient serum
R:Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thyse, H.; Grubb, A.; Adolf, G.
Eur. J. Haematol. 42, 270-275, 1989
A:Title: Isolation and characterization of a tumor necrosis factor binding protein from
A:Reference number: A60594; MUID:89171156
A:Accession: A60594
A:Molecule type: protein
A:Residues: 41-43, 'X', 45-53, 'V', 55-57, 'XK', 60 <OLS>
A:Experimental source: renal failure patient urine
R:Engelmann, H.; Novick, D.; Wallach, D.
Biol. Chem. 265, 1531-1536, 1990
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A:Reference number: A35010; MUID:90110215
A:Accession: A35010
A:Molecule type: protein
A:Residues: 41-45 <ENG>
A:Experimental source: normal urine
R:Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994
A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f
A:Reference number: JC2404; MUID:95128033
A:Accession: JC2404
A:Molecule type: protein
A:Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAJ>
A:Experimental source: urine
C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C:Genetics:
A:Gene: GDB:TNFR1
A:Cross-references: GDB:125913; OMIM:191190
A:Map position: 12p13.2-12p13.2
A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>
F:30-211/Domain: extracellular #status predicted <EXT>
F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status
F:44-82/Domain: NGF receptor repeat homology <NGI>

F:84-126/Domain: NGF receptor repeat homology <NG2>
F:127-167/Domain: NGF receptor repeat homology <NG3>
F:168-196/Domain: NGF receptor repeat homology <NG4>
F:212-234/Domain: transmembrane #status predicted <MEM>
F:235-455/Domain: intracellular #status predicted <INT>
F:34,145,151/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 99.0%; Score 1219; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.2e-82;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLLLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHPNNNSICT 60
DB 1 MGLSTVPDLLPLVLLLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHPNNNSICT 60

QY 61 KCHKGTLYNDPCPGQDTCRECEGSFTASENHLRCLSCSKCKRMGQVEISSCTVD 120
DB 61 KCHKGTLYNDPCPGQDTCRECEGSFTASENHLRCLSCSKCKRMGQVEISSCTVD 120

QY 121 RDTVCGCRKNQYRHWSENLFQCFNCSLCLNGTVHLSQEKONTVCTCHAGFFLENECV 180
DB 121 RDTVCGCRKNQYRHWSENLFQCFNCSLCLNGTVHLSQEKONTVCTCHAGFFLENECV 180

QY 181 SCNCKKSLECTKLCPLQIENYKGTEDSGTTVLLPLV 217
DB 181 SCNCKKSLECTKLCPLQIENYKGTEDSGTTVLLPLV 217